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Sequence 75 from Patent W00136632. AX147521 AX147521.1 GI:14346678 human.

Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalla, Eutheria, Primates, Catarrhini, Hominidae, Homo.
1 (bases 1 to 695)
Levine,Z., David,A., Azar,I., Khosravi,R. and Bernstein,J.
Variants of alternative splicing
Patent: WO 0136632-A 75 25-MAY-2001, REFERENCE AUTHORS TITLE JOURNAL

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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Bukaryota; Mutheria; Primates; Catarrhini; Hominidae; Homo.

(bases 1 to 868)

Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J.

Variantes of alternative splicing

Patent: WO 0136622-A 74 25-MAY-2001;

Compugen Ltd. (IL)
                                                                                                                                                               60 CTTGGGTCTGCCATCATGGATGTTCTCGCAGAAGCAAATGGCACTTTGCCTTAAACCTT 119
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0; Mismatches 106; Indels
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/db_xref="taxon:9606"
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Sequence 74 from Patent WO0136632.
AX147520 GI:14346677
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1302)
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120 TTGAAAACGCTGGGTAAAGACAACTCGAAGAATGTGTTTTTCTCACCCATGAGCATGTCC
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                                                                                                                                                                                                                                       240 ATACTTTCTTTCATAAAAGTGGCGGT----GGTGGAGACATCCACCAGGGCTTCCAGTCT
                                                       97 TIGAAAAAGCTAGGGGAAAACAACTCAAACAACTTATTTTTTC-CCCATGAGCATATCA
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Variants of alternative splicing
Patent: WO 013663-A 73 25-MAY-2001;
Compugen Ltd. (IL)
Location/Qualifiers
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Sequence 73 from Patent W00136632.
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/organism="Homo sapiens"
/db_xref="taxon:9606"
105 c 345 g 311
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Best Local Similarity 75.45
Matches 338; Conservative
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Sugano, S. and Suzuki, Y.

Sugano, S. and Suzuki, Y.

Direct Submission

Submission

Submitted (08-UUL-2002) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure, Human Genome
Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail:cdnal@ims.u-tokyo.ac.jp, Tel:81-3-5449-5286,

NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction and 5'-end one pass sequencing: Institute of Medical
Science, University of Tokyo, Laboratory of Genome Structure, Human
Genome Center; 3'-end one pass sequencing: RAB; clone selection for
full insert sequencing: RAB and Helix Research Institute.
                                                                                               ANDUBBE CONA PLUSSION TIN STANDA LINEAR PRI 15-JUL-2002 Homo mappiens CDNA PLUSSION Fis, Clone TST04708, highly similar to ANDREAT THROMBIN INHIBITOR.
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Homo sapiens testis cDNA to mRNA, clone_lib:TST clone:TST04708.
Homo sapiens
                                                                                                                                                                                                                                                                                                                        Oshima, A., Takahashi-Pujii, A., Tanase, T., Imose, N., Takeuchi, K. Arita, M., Musashino, K., Yuuki, H., Hara, H., Suzuki, Y., Hata, H., Nakagawa, K., Mizuno, S., Morinaga, M., Kawamura, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Nishikawa, T., Sugiyama, T., Kawakami, B., Nagai, K., Isogai, T. and Sugano, S.
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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35.2%; Score 248.4; DB 9;
Best Local Similarity 76.0%; Pred. No. 3.2e-60;
Matches 333; Conservative 0; Mismatches 101;
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/clone libe "TST"
/note="cloning vector:
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/clone="TST04708"
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Rosen, C.A., Cao, L., Adams, M.D. and Fuldner, R.A. Thrombin inhibitor.
Patent: US 613422-A 1 17-OCT-2000;
Location/Qualifiers
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Best Local Similarity 73.4'
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                     TCAGCCTTGGCCATGGTTTTCATGGGGGCAAAGGGAAACACTGCAGCTCCAGATGTCTCAG
                                                                           CTTCTTGTTGCAATTAACAGAACTGACTGCTAATATGTGCTTAGAACTGCCAACGGGCTC
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Pred. No. 9.1e-60;
); Mismatches 102;
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Best Local Similarity 75.8%;
Matches 332; Conservative (
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AKGNTAAQMAQILSFNKSGGGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSCDF
LSSFRDSCQFFYQABWEELDFISAVBKSRKHINWYABKTGFKALAELLSPGSYDPLTR
LLYUNAVYFKROWNGQPDFKNTEERLFKVSKNEEKPVQMFKQSTFKTJGEIFTQI
LVLPVYGKELMMIIMPDBTTDLRTVEKFYEKFVEWTRLDMFDEERVEYSTFTGI
EESYDMESVLRNLGMTDAFELGKADFSGMSQTDLSLSKVVHKSFVEWNEEGTEAAAAT
AAIMMMRCARFVPRFCADHPFLFFIQHRKTNGILFCGRFSSP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
Submitted (27-ARR-1993) Steinle A., University of Munich, Institute
of Immunology, Goethestrasse 31, W-8000 MUENCHEN 2, GERMANY
Location/Qualifiers
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Catarrhini, Hominidae, Homo.
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1 (bases 1 to 134)
Coughlin, P., Sun, J., Cerruti, L., Salem, H.H. and Bird, P.
Cloning and molecular characterization of a human intracellular serine proceinase inhibitor
Proc. Natl. Acad. Sci. U.S.A. 90 (20), 9417-9421 (1993)
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                          TAAAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACAACACGTGTAAAACTCCTGGG
                                                                                             653 regaggagerreactriareacececeragagagagereeagaaakeacaraaacacteeg
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/clone lib="cDNA in lamda gt11 (clontech)"
75. 1208
/function="serine proteinase inhibitor"
/citation=[1]
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Pred. No. 7e-60;
0; Mismatches 108; Indels
                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                 mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="thrombin inhibitor"
/protein_id="CAA80373.1"
/db_xref="GI:297412"
/db_xref="SWISS-PROT:P35237"
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="PTI/P"
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Steinle, A.
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PAT 08-JUN-2001
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                                                                                                                                               Homo sapiens
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eutele
Mammalia, Eutheria; Primates; Catarrhini, Hominidae, Homo
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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Levine, 2., David, A., Azar, I., Khosravi, R. and Bernstein, J. Variants of alternative splicing
Patent: Wo 0136632-A 62 25-MAY-2001;
Compugen Ltd. (IL)
Location/Qualifiers
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Pred. No. 9.1e-60;
0; Mismatches 102;
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Seguence 3028 from Patent WO0229103.
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/organism="Homo sapiens"
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Sequence 62 from Patent
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AX410381.1 GI:21443086
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Best Local Similarity 75.8%;
Matches 332; Conservative
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Eukaryota; Metazoa; (
Mammalia; Eutheria; )
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1 (1896) 1 to 1349)
Levine, Z., David, A., Azar, I., Khosravi, R. and Bernstein, J. Variante of alternative splicing
Patent: WO 0136632-A 22 25-MAY-2001;
Compugen Ltd. (IL)
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Sequence 22 from Patent W00136632.
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/organiam="Homo aapiens"
/db_xref="taxon:9606"
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Best Local Similarity 75.8
Matches 332; Conservative
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action with
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Catarrhini; Hominidae; Homo.
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GenBank staff at the National Library of Medicine created this
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Morgenstern, K.A.; Sprecher, C., Holth, L., Foster, D., Gran Ching, A. and Kisiel, W. Complementary DNA cloning and kinetic characterization of intracellular serine proteinase inhibitor: mechanism of trypsin and factor Xa as model proteinases
Blochemistry 33 (11), 3432-3441 (1994)
      Gene expression profiles in liver cancer Patent: WO 0229103-A 3028 11-APR-2002;
                                                                                                                                                                                                                                  4 ;
                                                                                                                                                                                                     Length 1465;
Mammalia; Butheria; Primates; Catarrhini; Hominidae;
                                                                                                                                             /note="EMBL/GenBank Accession No. S69272"
331 c 392 g 345 t
                                                                                                                                                                                                                                  Indels
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ilarity 75.8%; Pred. No. 9.1e-60;
Conservative 0; Mismatches 102
                                                                                                                  /organism="Homo sapiens"
/db_xref="taxon:9606"
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BC001394 linear PRI 12-JUL-2001 Homo sapiens, serine (or cysteine) proteinase inhibitor, clade B (ovalbumin), member 6, clone MGC:2180 IMAGE:3051381, mRNA, complete
                                                                                                                                                                                                                                                                                                                   /product="cytoplasmic antiproteinase"
/product="cytoplasmic antiproteinase"
/protein_id="AAB30320.1"
/db_xref="d1:546088"
/db_xref="d1:546088"
ACTINGACHAPACHALLKTLGKDNSKNVFFSPMSMSCALAMVYMGACTATION="MDVLAEANGTFALINLLKTLGKDNNKTGTQYLLRVANRLFGEKSCDFISSFROSCOKFYQAEMEELDFISAVEKSRKHINTWVAEKTEGKIAELLSPGSVDPLTRIJLVLVNAVYFRGNWDEQFDKENTEERLFKYSKNEEKPYQMMFKCYSTGEIFTQI
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EESYDMESYLRNLGMTDAFELGKADFSGMSQYDLSLSKVVHKSFVEVNBEGTEAAAAT
AAIMMMRCARFVPRFCADHPFLFFIQHSKTNGILFCGRFSSP"
331 c 392 g 345 t
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                                                                                                                                                                                                                 /gene="cytoplasmic antiproteinase, CAP"
/note="38 kda intracellular serine proteinase inhibitor;
This sequence comes from Fig. 1; CAP"
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the original journal article.
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                                                                                                                                                                          /gene="cytoplasmic antiproteinase, CAP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 246.8; DB 9;
Pred. No. 9.1e-60;
0; Mismatches 102;
                                                                                               /organism="Homo sapiens"
/db_xref="taxon:9606"
1. _1465.
  entry [NCBI gibbsq 145231] from
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Location/Qualifiers
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75.8%;
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Isogal.T. and Yanamoto, J.

Direct Submission

Direct Submission

Direct Submission

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7

Kazusa-Kamateri, Kisazazu, Chiba 292-0812, Japan

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center tec.); 5'- & 3'-end one pass sequencing: RAB; HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; Incation/Qualifiers
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highly similar
           CCATGGTCTACATGGGGGGAAAGGGAAACACCGCTGCACAGATGGCCCACATACTTTTTT 109
                                                                                               TTAGTAAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTTGTTG 285
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Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Satc),K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Satc),H., Wakamatsu,A., Ishii,S.,
Yamamotco,J., Isono,Y., Kawai,Hio,Y., Satco,K., Nishikawa,T.,
Kimura,K., Yamashita,H., Matsuv,K., Nakamura,Y., Sekine,M.,
Kakuchi,H., Murakawa,K., Kanahori,K., Takahashi-Fujii,A.,
Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S.,
Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
                                                                                                                                               410 TCAATAAAAGTGGCGGT---GGTGGAGACATCCACCAGGGCTTCCAGTCTTTTTTCACCG 466
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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Homo sapiens hippocampus cDNA to mRNA, clone_lib:BRHIP2
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clone BRHIP2011491,
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/clone_lib="BRHIP2"
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/organism="Homo sapiens"
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/clone="BRHIP2011491"
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Homo gapiens cDNA FLJ37664 fis,
to PLACENTAL THROMBIN INHIBITOR.
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ORIGIN
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AK094983
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: "Isc mgonhgri.nlh.gov
Shevchenko,Y., Wetherby,K.D., Backstrom-Sternberg,S.M.,
Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S.,
Dietrich,N.L., Guan,X., Gupta,J., Ho.S.-L., Karlins,E., Legaspi,R.,
McDowell,J., Pearson,R., Snyder,B., Stantripop,S., McCloskey,J.C.,
Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A.,
Zhang,L.-H. and Green,R.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at: http://image.llnl.gov Series: IRAL Plate: 4 Row: m. Column: 23
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 546087.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="serine (or cysteine) proteinase inhibitor, clade 8 (ovalbumin), member 6" protein id="AAH01394.1" /db_xref="GI:12655087"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         / translation="MDVIAEANGTFALNILKTLGKDNSKNVFFSPMSNSCALAMYYMG
AKGNTAAQMAQILSFNKSGGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSCDF
AKGNTAAQMAQILSFNKSGGGDIHQGFQSLLTEVNKTGTQYLLRVANRLFGEKSCDF
ALSFRNSCQKFYQAEMSELDFISAVEKSRKHINTWVAEKTAEKTAELLSPGSVDPLTR
LVLVNAVYFRGWWDEOFDKENTEERLFKVSKNBEKPVQMFKKGSTFKKTYIGELFTQI
LVLPYYGKELMNITMLDPBTTDLRTVEKELTYEKFVBMTRLDMNDEEEVBSLPRFKL
BESYDMESVLRNLGMTDAFELGKADFSGMSQTDLSLSKVVHKSFVEWNEEGTERAAAAT
AAIMWRRCARFVPRFCADHPFLFFIGHSKTNGILFCGRFSSP"
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                                     Euteleostomi;
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                                                                                                 Strausberg_R.
Direct Submission
Submission
Submission
Submitted (12-DEC-2000) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCGTCATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGC
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                                                                                                                                                                                                                                                                                                                                                                          CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC).
Galthersburg, Maryland;
                               Craniata; Vertebrata; Eutele
Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue type="Colon, adenocarcinoma"
/clone_lib="NIH MGC_15"
/lab_host="DH10B-R"
                                                                                                                                                                                                                                                                     NIH-MGC Project URL: http://mgc.nci.nih.gov
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Best Local Similarity 75.8%; Pred. No. 9.1e-60;
Matches 332; Conservative 0; Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /db_xref="LocusID:5269"
/db_xref="taxon:9606"
/clone="MGC:2180 IMAGE:3051381"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       http://www.nisc.nih.gov/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/db_xref="LocusID:5269"
                            Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
1 (bases 1 to 1523)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note="Vector: pOTB7"
                                                                                                                                                                                                                                                                                               Contact: MGČ help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
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/codon start=1
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Isogai, T., Otsuki, T. and Sugiyama, T.

Direct Submission

Submission

Submitted (24-0CT-2001) Takeo Isogai, Helix Research Institute,
Submitted (24-0CT-2001) Takeo Isogai, Helix Research Institute,
Genomics Laboratory; 1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)

NEDO human DNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; ODNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRI 01-AUG-2002
highly similar
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                         774 ccarcarddargrichtcacagaadgaaarggcacrirgccriaaaccrirgaaaacac
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                                                                                             47 CCGTCATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGC
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                                                 4; Gaps
Length 2036;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mRNA linear
clone SPLEN2000247,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             insert sequence).
to mRNA, clone_lib:SPLEN2
                                                 Indels
Score 246.8; DB 9;
Pred. No. 9.2e-60;
0; Mismatches 102;
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gai,T., Otsuki,T. and Sugiyama,T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AKO57138
3271 bp
Homo sapiens cDNÄ FLJ32576 fis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ragergaaaagacagaag 1208
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Homo sapiens spleen cDNA
clone:SPLEN2000247.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AK057138.1 GI:16552727
     35.0%;
75.8%;
                                                      332; Conservative
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                               Similarity
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          Query Match
Best Local
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AK057138
                                                           Matches
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LOCUS

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Homo sapiens CDNA: FLJ23496 fis, clone LNG02535, highly similar to S69272 human mRNA for cytoplasmic antiproteinase=38 kda akto27149
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AK027149.1 GI:10440203
AK027149.1 GI:10440203
oligo capping; fis (full insert sequence).
Home sapiens human lung cDNA to mRNA, clone_lib:LNG clone:LNG02535.
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Sugano, S., Suzuki, Y., Ota, T., Obayashi, M., Nishi, T., Isogai, T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    2235 AAGTGAACAAGACTGGCACGCAGTACTTGCTTAGGATGGCCAACAGGCTCTTTGGGGAAA
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Evaluation; clone selection for full insert sequencing: RAB HRI.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                  Length 3271;
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Pred. No. 9.2e-60;
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/clone_lib="splen"
/note="cloning vector: pV
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75.8%;
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Best Local Similarity 75.8
Matches 332; Conservative
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Shibahara, T., Tanaka, T. and Nakamura, Y.

Direct Submission

Submitted (129-AuG-2000) Sumio Sugano, Institute of Medical Science,
University of Tokyo, Laboratory of Genome Structure Analysis,
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Genome Center; Shirokane-dai, 4-6-1, Minato-ku, Tokyo 108-8639,
Rax:81-3-5449-5416)

NEDO human cDNA sequencing project supported by Ministry of
International Trade and Industry of Japan; cDNA full insert
sequencing: Research Association for Blotechnology; cDNA library
Vivology and Human Genome Center, Institute of Medical Science,
University of Tokyo (partly supported by Science and Technology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. 2759
Thote="highly similar to 569272 human mRNA for cytoplasmic antiproceinase=38 kda intracellular serine proteinase inhibitor."
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29-FEB-2000; 2000WO-US05082.

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## ALIGNMENTS

RESULT 1 AAA64690

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Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia; cardiovascular disorder; cardiorare; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; epithelial cell proliferation; skin aging; sunburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative; 89.
                                                                                                                                                                                                                                                                  /*tag= a
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/note= "Xaa is any L-amino acid"
                                                                           Nucleotide sequence encoding a human serpin polypeptide.
                                                                                                                                                                                                                                         Location/Qualifiers
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AAA64690 standard; DNA; 706
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                          AAA64690;
                                                                                                                                                                                                                Ношо
                                                                                                                                                                                                                                         Key
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The present sequence encodes a human serpin polypeptide. Serpin is a member of the serine protease inhibitor superfamily of polypeptides.

The serpin polynucleotides and polypeptides are used to prevent, treat or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats, for ameliorate a medical conditions in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or Sheep. Disorders which are diagnosed or treated include autoimmune disease e.g. rheumatoid arthritis, cardiovascular disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. nervous system disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to rapporting cell culture of primary tissues, to transplantation, for supporting cell culture of primary tissues, to crement a food additive or preservative to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGICALGATACACAGAGAGTCCACACACGTGTAAACTCCTGGGTTGCTGATAAAACTA 480
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                                                                                                                                                                                                                                                                                                                                                                                        Novel human serine protease inhibitor superfamily of proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the Serpin polypeptides
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 706;
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Pred. No. 8.3e-199;
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100.0%;
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99US-0124094.
99US-0149452.
                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
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12-MAR-1999;
                                                                                                18-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated serine protease inhibitor polypeptide for treating, preventing and/ or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis
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                                                                              cciciidinacidedaageengeeniicaeageeenacideiicaeicaiiideeaaa
                                                                                                        CCTCTTGTTACTGCAAAGCCTGCCTTTCACAGCCCCTACTGGTTCACTCTATTCCCAAAT
AAGCCTGGAAAATTATTCAAACAAGCCTGTCACATCTGGAGGAGCCAGGAATCGCCTCTT
                                                                                                                                                                                                                                                                                                                                           Human serine protease inhibitor (serpin) coding sequence HMCIS41.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Transl except= (pos:632..635, aa:Xaa)
/note= "No start codon is given; Xaa is unknown"
                                                                                                                                                                                                                                                                                                                                                                  Human, serine protease inhibitors; serpin; blood coagulation; proteinase-activated physiological process; gene therapy; antisense therapy; cancer; inflammation; neurological disease; immune disease; gene; ss; HMCIS41.
                                                                                                                                                                               Location/Qualifiers
3.650
4.450
/ partial
/product = "Human serpin protein HMCIS41"
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29-FEB-2000; 2000WO-US05082.
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cardiovascular disorder; cardiac arrest; cerebrovascular disorder; anglogenesis; nervous system disorder; Albheimer's disease; infection; ocular disorder; corneal infection; epithelial cell proliferation; skin aging; subburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative; 88.

/transl\_except= (pos: 583..585, aa: Xaa)
/product= "serpin"
/note= "Xaa is any L-amino acid; no termination codon given"

Location/Qualifiers

sapiens

Homo Key ø

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DNA and amino acid sequences of the invention are useful in the treatmen (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present cDNA sequence represents a human serpin coding sequence of the
                                                                                                                                                              CTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAACAAC
                                                                                                                                                                                                                                                               TCAAACAACTTATTTTTTTCCCCATGAGCATATCATCAGGCCTTGGCCATGGTTTTCATGG
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                                                                                                  Score 704; DB 23; I Pred. No. 8.3e-199;
                                                                                                                          Mismatches
                                                                                        99.7%; Scc.
100.0%; Pred
                                                                                                                        Conservative
                                                                                                            Similarity
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Novel human serine protease inhibitor superfamily of proteins useful for diagnosing, treating, preventing and/or prognosing disorders related to the Serpin polypeptides

99US-0122276. 99US-0124094. 99US-0149452.

2000WO-US05082

29-FEB-2000;

01-MAR-1999; 12-MAR-1999; 18-AUG-1999;

WO200052160-A1

08-SEP-2000

(HUMA-) HUMAN GENOME SCI INC

WPI; 2000-579284/54. P-PSDB; AAB08783.

Ruben SM, Ni J;

Claim 1; Page 12-13; 215pp; English

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The present sequence encodes a human serpin polypeptide. Serpin is a member of the serine protease inhibitor superfamily of polypeptides. The serpin polymorlectides and polypeptides are used to prevent, treat or amaliorate a medical conditions in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, treated include autoimmune diseases e.g. rheumatoid arthritis, cardiovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
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99.0%; Pred. No. 9.7e-164;
iive 0; Mismatches 0;
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Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia;

Nucleotide sequence encoding a human serpin polypeptide.

(first entry)

02-JAN-2001

AAA74934 ID AAA7 XX XX XX DT 02-1 XX 
AAA74934;

BP

AAA74934 standard; DNA; 599

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neurological diseases and also for testing and detection e.g. diagnosis
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Matches 598; Conservative
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                                       AAAATCGGAAGCTGAAGATGGAGATATTCATCGAGGTTTTTCAGTCACTTCTTGTTGCAATT
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                                                                                                                                                                                                                                                                   Human, serine protease inhibitors; serpin; blood coagulation; proteinase-activated physiological process; gene therapy; antisense therapy; cancer; inflammation; neurological disease;
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/*teg= a
/*product= "Human serpin protein 1"
/transl except= (pos:583..585, aa:Xaa)
/note= "Xaa is unknown"
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29-FEB-2000; 2000WO-US05082.
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P-PSDB; AA014921.
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                                          The invention comprises the amino acid and coding sequences of a group of novel human serine protease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and 100 kDa in molecular mass. The majority of serpins function as protease activated physiological processes (e.g. blood coagulation. The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present cDNA sequence represents a human serpin coding sequence of the
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Pred. No. 8.7e-164;
0; Mismatches 0; Indels
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Page 14-15; 288pp; English
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                                               Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm rheumatoid arthitis; hyperproliferative disorder; cerebral ischemia; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; epithelial cell proliferation; skin aging; sunburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative; ss.
                                                                                                                                                                                                                                                                                                                                                                               /transl_except= (pos: 91..93, aa: Xaa)
/transl_except= (pos: 94..96, aa: Xaa)
/transl_except= (pos: 97..99, aa: Xaa)
/product= "serpin"
/note= "Xaa is any L-amino acid; no termination codon
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99US-0124094.
99US-0149452.
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P-PSDB; AAB08784.
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12-MAR-1999;
18-AUG-1999;
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           61 GAAAACAACTCAAACAACTTATTTTTCCNNNNNNNNCCCATGAGCATATCATCAGGCC 120
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                                           TTGGCCATGGTTTTCATGGGGCAAAGGGAAACACTGCAGCTCAGGCACTT
                                                                                     TGTTTTAGTAAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTT
                                                                                                                               GTTGCAATTAACAGAACTGACACTGAATATGTGCTTAGAACTGCCAACGGGCTCTTTGGA
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                                                                                                                                                                                                                                                                                                             GAAAAGTCTTATGATTTCCTCACAGGTTTTACAGATTCCTGTGGCAAATTCTACCAAGCA
                                                                                                                                                                                                                                                                                                                                  Human, serine protease inhibitors; serpin; blood coagulation; proteinase-activated physiological process; gene therapy; antisense therapy; cancer; inflammation; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human serine protease inhibitor (serpin) coding sequence 2.
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/transl_except= (pos:91..96, aa:xaa)
/transl_except= (pos:97..99, aa:xaa)
/transl_except= (pos:592..594, aa:xaa)
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1..606
/*tag= a
/product= "Human serpin protein 2"
GAAAACAACTCAAACAACTTATTTTTC----
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582

Ruben SM, P-PSDB; AAO14922 Ni J, XKKX4XIXKKXXIIIIIXXXXX0000

The invention comprises the amino acid and coding sequences of a group of novel human serine procease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and 100 kba in molecular mass. The majority of serpins function as protease inhibitors and so are involved in the regulation of several proteinase-activated physiological processes (e.g. blood coagulation). The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The Isolated serine protease inhibitor polypeptide for treating, preventing and/ or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis present cDNA sequence represents a human serpin coding sequence of the Claim 1; Page 15; 288pp; English. (HUMA-) HUMAN GENOME SCI INC 28-JAN-2000; 2000US-0178769 29-FEB-2000; 2000WO-US05082 ; Shi 2001-457730/49.

Sequence 608 BP; 171 A; 141 C; 122 G; 164 T; 10 other;

52 ATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAAACCTTTGAAAAAGCTAGGG 111 161 9 1 ATGGATGCTCTATCAGAAGCAAATGGCACAITTGCAITAAACCTTTTGAAAAAGCTAGGG 112 GAAAACAACTCAAACTTATTTTTTC-----CCCATGAGCATATCATCAGCC Gaps 10; Score 577; DB 23; Length 608; Pred. No. 4.1e-161; 0; Mismatches 0; Indels 10 0 81.7%; nilarity 98.4%; Conservative 0 Query Match Best Local Similarity Matches 598; Conserv ò g ò

TTGGCCATGGTTTTCATGGGGGAAAGGGAAACACTGCAGCTCAGATGTCTCAGGCACTT 61 162

Treeccarectricarececcaaegeaaacacrecaecreagarercreagecacrr TGTTTTAGTAAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTT 181 İGİTTIAĞIAAAAICGGAĞGIĞAAGAIĞGAĞAIAAITCAICGAĞĞITITCAĞICACITCIT 121 222

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301 GAAAAGTCTTATGATTTCCTCAGGTTTTTACAGATTCCTGTGGCAAATTCTACCAAGCA 361 ACGATAAAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACAACACGTGTAAACTCC TGGGTTGCTGATAAAACTAAAGCCTGGAAAATTATTCAAACAAGCCTGTCACATCTGGAG GAAAAGTCTTATGATTTCCTCACAGGTTTTACAGATTCCTGTGGCAAATTCTACCAAGCA ACGATAAAACAGCTAGGACTTTGTGAATGATACAGAGAAGTCCACAAACACGTGTAAAACTCC 402 342

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Human; gene; ss; inflammatory condition; shock; sepsis; immune response; cancer; wound healing; central nervous system disease; haematopoiests; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; platelet disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder; Wang J, Asundi V, ď Zhou l RT; Liu C, Drmanac 1 뭠. Human novel polynucleotide #78. ABK94967 standard; cDNA; 943 30-NOV-2001; 2001WO-US47004 30-NOV-2000; 2000US-0028952 (first entry) Goodrich RW, 649 608 (HYSE-) HYSEQ INC. TCCCTGTG fungal infection WO200244340-A2. Homo sapiens Tang YT, Go Yamazaki V, 30-AUG-2002 06-JUN-2002 ABK94967; 642 601 RESULT 7 **ABK94967** g g à

Novel nucleic acids and polypeptides for diagnosis, treatment inflammatory, autoimmune, nervous system, myeloid or lymphoid disorders, cancer and promoting wound healing -

WPI; 2002-508509/54.

P-PSDB; ABG66743.

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Claim 1; Page 524-525; 672pp; English.

The invention relates to human novel polynucleotides are useful for polypeptides. The polynucleotides and polypeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's treating inflammatory conditions such as arthritis, nephritis, Crohn's cand cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and converted thissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, parkinson's disease, Huntington's disease and amyotrophic lateral sclerosis. The sequences are involved in chemctactic or chemokrietic activity, regulation of haematopoiesis, treatment of myeloid or lymphoid coll disorders and platelet disorders such as thrombocytopenia, calivity, issue repair, healing of burns, incisions, ulcers, treatment of growth, tissue repair, healing of burns, incisions, ulcers, treatment of disease. The sequences of the invention are also useful for gut disease. The sequences of the invention are also useful for gut protection or regeneration and treatment of lung or liver fibrosis, reperfusion injury in various tissues; immune deficiencies and disorders including severe combined immunodeficiency (SCID), bacterial or fungal infections, autoimmune disorders e.g. multiple sclerosis and myasthenia

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; prostate cancer; prostate cancer antigen; detection; diagnosis; neuroprotective; cytostatic; cardioactive; immunomodulatory; muscular; vulnerary; gastrointestinal; nephrotropic; antilnfective; gynaecological; antibacterial; gene therapy; neural; immune; reproductive; renal; gastrointestinal; pulmonary; cardiovascular; proliferative disorder; wound; infectious disease; ss.
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gravis, allergic conditions such as asthma, thrombolysis or thrombosis and coagulation disorders. Sequences ABK94890-ABK94982 represent human
                                                                                                                                                CTTCGCTCCTGGGCAGCTGCGCGGAGAACTGGGGCTCACCGTCATGGATGCTCATCAGA
                                                                                                                                                                                                CTTATITITICCCCA-TGAGCATATCATCAGCCTTGGCCATGGTTTTCATGGGGGCAAA
                                                                                                                                                                                                                                                  CTTATTTTTTCCCCACTGAGCATATCATCACCCTTGGCCATGGTTTTCATGGGGGCAAA
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                                                                                                        Gaps
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                                                                                                        1,
                                                                              943;
                                                                             24; Length
                                                                                                      7; Indels
                                                  Sequence 943 BP; 271 A; 214 C; 186 G; 272 T; 0 other;
                                                                                         Pred. No. 4.2e-127;
0; Mismatches 7;
                                                                              DB
                                                                             Score 462.8;
             and coagulation disorders. Sequences AB novel polynucleotides of the invention.
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                                                                         65.6%;
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Matches 478; Conservative
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12-MAR-1999;

08-MAR-2000; 2000WO-US05988

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21-SEP-2000

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              proteins, called prostate cancer antigens, given in AAB56363 to AAB57302. The prostate cancer antigens can have neuroprotective, cytostatic, cardioactive, immunomodulatory, muscular, vulnerary, gastrointestinal, nephrotropic, antiinfective, gynaecological and antibacterial activities, and can be used in gene therapy. The prostate cancer antigen polymuclectides may be used for detection of prostate cancer, chromosome identification, as chromosome markers, and for numerous other diagnostic
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                                                                                                                                                                                                                                                                         Prostate cancer associated gene sequences, referred to as prostate cancer antigens, useful for treatment, prevention, and diagnosis of disorders such as prostate cancer -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAF15566 to AAF16505 encode the human prostate cancer associated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 251.2; DB 21; Length 1624; Pred. No. 3.9e-64;
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P-PSDB; AAB56862.
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AAS06075;

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The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor. Granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasocative intestinal polypeptide receptor 2. The polypeptides and their sesociated nucleic acids are useful for identification of variant sesociated nucleic acids are useful for identification of variant molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular chembritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidoric pulmonary granulomatous diseases such as asbestosis and vascular including candinary granulomatous diseases such as asbestosis and vascular including candinary granulomatous diseases such as asbestosis and vascular
                                                                                                                            Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; ds; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                  nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
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                                                                                      DNA #75.
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                                                                                   Angiotensin converting enzyme (ACEV) splice variant
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Pred. No. 4.5e-64;
0; Mismatches 106;
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Best Local Similarity 75.4%;
Matches 338; Conservative
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P-PSDB; AAU02975.
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10-DEC-1999;
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eplice variant (ACEV) polypeptide. The polypeptides of the invention findlude variants of granulocyte colony stimulating factor receptor, dincarde variants of granulocyte colony stimulating factor receptor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and wasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such diseases such as thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic parthylories includent as sebetosis and vascular complex parthylories.
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Pred. No. 5e-64;
0; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 868 BP; 214 A; 212 C; 227 G; 215 T; 0 other;
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Best Local Similarity 75.4%;
Matches 338; Conservative (
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416 455 CAAGCAGAGATGGAGGAGCTTGACTTTATCAGGGCGCGTAGAGAGTCCAGAAAACACATA 476 Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; glatelet-detived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; ds; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; Tricogadadactricrodriticorcionerritias CAAGCAACGATAAAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACAACACGTGTA Angiotensin converting enzyme (ACEV) splice variant DNA #73. AACTCCTGGGTTGCTGATAAAACTAAAG 483 AACACCTGGGTAGCTGAAAGACAGAAG 504 ВР AAS06073 standard; DNA; 1302 (first entry) 12-SEP-2001 357 396 417 456 477 AAS06073; AAS06073

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97 TTGAAAAAGCTAGGGGAAAACAACTCAAACAACTTATTTTTC-CCCATGAGCATATCA 155

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CTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTT

35.5%; Score 250.4; DB 22; Length 1302; 75.4%; Pred. No. 6.1e-64; tive 0; Mismatches 106; Indels 4;

Best Local Similarity 75.4 Matches 338; Conservative

Query Match

37

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Sequence 1302 BP; 341 A; 305 C; 345 G; 311 T; 0 other;

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CTTCTCACCGAAGTGAACAAGACTGGCACGCAGTACTTGCTTAGGATGGCCAACAGGCTC 356

CTTCTTGTTGCAATTAACAGAACTGACACTGAATATGTGCTTAGAACTGCCAACGGGCTC

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The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony esimulating factor receptor.

Cinclude variants of granulocyte colony esimulating factor receptor, glucagon, interleukin 6, platelate-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex complicities, multiple seletosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as such as such as such as such as such as such as such as such as such as such as such as such as such as immune complex pathologies involving an endothelial abnormality such as deep vein
multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a thrombin inhibitor. This is useful for diagnosis and treatment of thrombosis, neurodegenerative diseases uch as Alzheimer's disease and Parkinson's disease, tumor metastasis, to prevent proximal extension of deep venous thrombosis or the recurrence of pulmonary embolisms and also to treat risk patients who have congestive heart failure, acute myocardial infarction or cardiomyopathy to prevent the development of deep vein thrombosis or pulmonary embolism. The thrombin inhibitor is also useful for screening chemical compounds that either up or down regulate its
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                                                                                     CAAGCAACGATAAAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACAACACGTGTA
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Pred. No. 1.4e-63;
1; Mismatches 120; Indels
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Best Local Similarity 73.4%;
Matches 345; Conservative
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The thrombin inhibitor may be used therapeutically or diagnostically to treat or prevent diseases related to thrombosis characterized by hypercoaquiation of cells. The protein may also be used to prevent extension of deep venous thrombosis of the recurrence of pulmonary embolisms and recurrence of cerebral or other systemic embolisms, to treat high risk
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160 ITTCTCACCCATGAGCATGTCCTGTGCCTGGCCATGGTCTACATGGGGGCAAAGGGAAA
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vascular disorder; asbestosis.

WO200136632-A2 Homo sapiens.

25-MAY-2001

17-NOV-2000; 2000WO-IL00766.

99IL-0132978 99IL-0133455

17-NOV-1999; .0-DEC-1999; (COMP-) COMPUGEN LTD.

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Datients, e.g. those who have congestive heart failure, acute myocardial infarction or cardiomyopathy to prevent the development of deep vein thromboasis or pulmonary embodism, and as long term therapy for occasional patient who has recurrent thrombosis or embolism while on the drug cumor metasteases, excrinoma of the brain, liver, lung, bone and neoplastic plasma cell carcinoma, and neurodegenerative diseases (e.g. Alzheimer's or Parkinson's disease). It can also be used against clot-bound thrombin, which produces clot accretion, for screening clot-bound thrombin, which produces clot accretion, for screening producing antibodies. The thrombin inhibitor can be used as pharmaceutical to mammals, such as humans, mice, rate; hamster, dogs, rabbits and cats. The CDNA sequences of the thrombin inhibitor may be
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Sequence 1366 BP; 360 A; 332 C; 355 G; 317 T; 2 other;

75 TGGCACATTTGCATTAAACCTTTTGAAAAGGTAGGGGAAAAGAACTGAAACAACTTATT 134 135 TTTTC-CCCATGAGCATATCATCAGCCTTGGCGATGGTTTTCATGGGGGAAAAGGGAAA 193 253 carcacaegerrecaerterrereaceaagreaacaaeaeregecaegeaerr 336 GCTTAGAACTGCCAACGGGCTCTTTGGAGAAAGTCTTATGATTTCCTCACAGGTTTTAC 373 74 rrcrecrescrescrescrerers da de la contra del la contra del la contra del la contra del la contra del la contra de la contra de la contra del la co TCCTGGGCAGCTGCGGGGAGAACTGGGGCTCACCGTCATGGATGCTCTATGAGAAGCAAA 100 rescarritecerradacerritedada cacressina de caracacado de conservado CACTGCAGCTCAGATGTCTCAGGCACTTTGTTTTAGTAAAATCGGAGGTGAAGATGGAGA 254 TATTCATCGAGGTTTTCAGTCACTTCTTGCAATTAACAGAACTGACACTGAATATGT 4; Gaps Score 249.2; DB 22; Length 1366; Pred. No. 1.4e-63; 1; Mismatches 120; Indels 4; AGAGAAGTCCACAACACGTGTAAACTCCTGGGTTGCTGATAAAACTAAAG 483 iry Match
 Local Similarity 73.4%;
chee 345; Conservative 1 15 6 374 194 397 434 g ઠે ò g g ઠે ò 유 ઠે g ò

AGATTCCTGTGGCAAATTCTACCAAGCAACGATAAAACAGCTAGACTTTGTGAATGATAC 433 Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endotherial cell growth factor; cardiovascular disease; callular tumour antigen P53; cyclin-dependent kinase inhibitor. 1C; ds; myocardial infarction; oxonary arterial thrombosis; renal disease; myocardial infarction; coronary arterial thrombosis; renal disease; dashetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; Angiotensin converting enzyme (ACEV) splice variant DNA #63. AAS06063 standard; DNA; 1324 BP. (first entry) 12-SEP-2001 

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The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, colondariants of granulocyte colony stimulating factor receptor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen PS3, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment as attentions of various disorders including cardiovascular diseases such as attentions and diseases such as diabetic nephropathy, mmuscular diseases such as hypertrophy, immune disorders such as immune complex complexity, multiple selerosis, cancer, sarcoldesis, nonarcoldetic complexity.
                                                                                                                                                                                                                                                                                                                                                                                    Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
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pathologies involving an endothelial abnormality such as deep vein
                                                                                                                                                                                                                                                                                            Khosravi R, Bernstein J;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 1; Page 360; 519pp; English.
                                                                                                                                                                                                                                                                                        Levine Z, David A, Azar I,
                                                                                                                                                                                                                                                                                                                           WPI; 2001-336004/35
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4; Gaps Score 246.8; DB 22; Length 1324; Pred. No. 7.2e-63; 0; Mismatches 102; Indels 4; Query Match
Best Local Similarity 75.8%;
Matches 332; Conservative

225 263 165 323 47 CCGTCATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGC 107 TAGGGGAAAACAACTCAAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG 441 AAGTGAAGAAGACTGGCACGCAGTACTTGCTTAGGGTGGCCAACAGGCTCTTTGGGGAAA 204 ccarcardardrichcecadaadcaaarddacacrirdccriraaaccriricaaaaaccc 166 CCATGGTTTTCATGGGGCAAAGGGAAACACTGCAGCTCAGATGTCTCAGGCACTTTGTT 384 icharhahagrescer---estesakahararcakeasesarresakirerintranes 286 CAATTAACAGAACTGACACTGAATATGTGCTTAGAACTGCCAACGGGGTCTTTGGAGAAA 226 ITAGTAAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTTGTTG ò 임 ò g ò 셤 ò g g ò

AGTOTTATGATTTCCTCACAGGTTTTACAGATTCCTGTGGCAAATTCTACCAAGCAACGA 405

4; Gaps

DB 22; Length 1349;

T; 0 other;

Sequence 1349, BP; 370 A; 298 C; 358 G; 323

thrombosis

S X G

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granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen p53; cyclin-dependent kinase inhibitor 1C; ds; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; multiple sclerosis; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
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                                                                     sei regaggaderreachtrarcaggeeegragagaagreeagaaaacacaraaaceeerge
501 AGTCTTGTGATTTTCCTCTCTTTTAGAGATTCCTGCCAAAAATTCTACCAAGCAGAGA 560
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                     TAAAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACAACACGTGTAAACTCCTGGG
                                                                                                                                                                                                                                                                                                                                                                             splice variant; ACEV; interleukin 6;
                                                                                                                                                                                                                                                                                                                                          Angiotensin converting enzyme (ACEV) splice variant DNA #22.
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                                                                                                                                                                                                                                      AAS06022 standard; DNA; 1349 BP
                                                                                                                                                621 radcrchahahahaha 638
                                                                                                                TTGCTGATAAAACTAAAG 483
                                                                                                                                                                                                                                                                                                                                                                                   Angiotensin converting enzyme
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10-DEC-1999;
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The sequence represents a DNA encoding an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of gramulocyte colony stimularing factor receptor. Glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant captures and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and adagnosis of various disorders innoluding cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex chemicals, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pathologies involving an endothelial abnormality such as deep vein

Claim 1; Page 327; 519pp; English

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35.0%; Score 246.8; DB 22; Length
75.8%; Pred. No. 7.2e-63;
tive 0; Mismatches 102; Indels
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                        Query Match 35.0
Best Local Similarity 75.8
Matches 332; Conservative
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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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US-07-266-910-1

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US-08-474-661-30
US-08-611-977-30
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                                                                                                                                                        IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
                                                                                                                                                                                                                                                                                                                      Issued_Patents_NA:*
                                                                                                                                                                                                                                    Minimum DB seq length: 0
Maximum DB seq length: 200000000
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                                                                                                                                                         Scoring table:
                                          OM nucleic
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                                                                                                                                   Sequence:
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                                                                 Run on:
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<u>ښ</u> Appl Appli Appli Appli Appli Appli Appli Appli Appli Sequence 382, Sequence 382, Sequence 382, Sequence 11, Ag Sequence 11, Ag Sequence 2, Ag Sequence 2, Ag Sequence 6, Ag Sequence 6, Ag Sequence 6, Ag Sequence 11, Ag Sequence Gaps 4 Sequence 1, Application US/09200965
Patent No. 6133422
GENERAL INFORMATION:
TILLE OF INVENTION: Thrombin Inhibitor
NUMBER OF SEQUENCES:
CORRESPONDENCES:
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER: 1BM PS/2
OMPUTER: 1BM PS/2
COMPUTER: WRO DERFECT 5.1
CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
FILLED OF INVENTABLES IN US OF SERVER STATE
COMPUTER: 1BM PS/2
COMPUTER: 1BM PS/2
COMPUTER: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
FILLED OF SEATHER STATE
COURTER IN WORD PERFECT 5.1
CURRENT APPLICATION DATA: Query Match 35.3%; Score 249.2; DB 3; Best Local Similarity 73.4%; Pred. No. 1.1e-65; Matches 345; Conservative 1; Mismatches 120; US-09-605-785-382 US-09-439-113-382 US-07-768-286B-1 US-07-911-531-18 US-07-691-565A-18 US-09-023-461-1 US-09-033-556-3 US-09-29-141-4 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 US-09-299-141-1 ALIGNMENTS FILING DATE:
CLASSIPICATION:
PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/171,817
FILING DATE: 22-DECEMBER-1993
ATTORNEY/AGENT INPORMATION:
NAME: FERRARO, GREGORY D.
REGISTRATION NUMBER: 36,134
REPERROKO/DOCKET NUMBER: 325800-47
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-994-1700
TELEPRX: 201-994-1704
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1366 BASE PAIRS LENGTH: 1366 BASE PAIRS TYPE: NUCLEIC ACID STRANDEDNESS: SINGLE 1610 2409 12040 12047 12047 12047 1208 6142 6565 6714 6924 6924 6924 TOPOLOGY: LINEAR MOLECULE TYPE: CDNA

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Sequence

Sequence Sequence

Sequence

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270 T----
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FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                               US-08-464-148-1
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                                                                               100 -TGGCACCTTTGCCTTAAACCTTTGAAACACTGGGTAAAGACAACTCGAAGAATGTGTT 159
                                                                                                                      135 TTTTTC-CCCATGAGCATATCATCACCTTGGCCATGGTTTTCATGGGGGCAAAGGGAAA 193
                                                                                                                                                              160 rrrcrcacccardadcarcrcrcrcrcrccrcccardcrcracardadadedeaaa 219
                                                                                                                                                                                                     253
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                                           TGGCACATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAACAACTCAAACAACTTATT 134
  40 ITCIGCTCGCTCCCCGCTCTGGAGTCTGCCATCATGGATGTTCTCGCAGAAGCAAA 99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
THILE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
CORRESPONDENCE SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                     CACTGCAGCTCAGATGTCTCAGGCACTTTGTTTTAGTAAAATCGGAGGTGAAGATGGAGA
                                                                                                                                                                                                                                           220 caccecrecacadardecccadaracriricirircaaraaradecedre---Greeada
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COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/NS-DOS

COMPUTER: APELICATION DATA:

APPLICATION NUMBER: US/08/464,148

FILLING DATE: 05-UN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-FBB-1995
ATTONNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,995
REFERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1, Application US/08464148
Patent No. 5710026
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INFORMATION FOR SEQ ID NO: 1:
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nucleic acid
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
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TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES:
TOWNERS OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         226 TIAGIAAAATCGGAGGTGAAGATGGAGATATTCATCGAGGTTTTCAGTCACTTCTTTC
                                                                                                                                                                                                                                                                   TGATGGATGACTCTGTGAAGCAAATGGCACTTTTGCCATCAGCTTATTAAAATATTGG
                                                                                                                                                                                                                                                                                                                                                                                                                                    CCATGGTTTTCATGGGGGCAAAGGGAAACACTGCAGCTCAGATGTCTCAGGCACTTTGTT
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                                                                                                                                                                                                                                                                                                                               GGGAAA---ACAACTCAAACAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGG
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                                                                                                                                                                            16;
                                                                                                                          Length 1425;
                                                                                                                                                                            Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
                                                                                                                             DB 1;
                     /product= "CYTOPLASMIC
ANTIPROTEINASE-2 PROTEIN"
                                                                                                                                                   Pred. No. 3.8e-55;
0; Mismatches 101
                                                                                                                             Score 214.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CIASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: PARTELEE, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-385-500-1
; Sequence 1, Application US/08385500
Patent No. 5712117
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TGCCAGAGAGACTGAAG 515
                                                                                                                          Query Match 30.4%;
Best Local Similarity 73.3%;
Matches 321; Conservative (
LOCATION: 92.1213
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94105-1493
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90 TGATGGATGACCTCTGTGAAGCAAATGGCATTTTTGCCATCAGCTTATTAAAATATTTGG 149
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                    SYSTEM: PC-DOS/MS-DOS
Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.4%; Score 214.4; DB 1; 73.3%; Pred. No. 3.8e-55; iive 0; Mismatches 101;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION: 92..1213
OTHER INFORMATION: /product= "CYTOPLASMIC OTHER INFORMATION: ANTIPROTEINASE-2 PROTEIN"
                                                     SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION: 435
                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/385,500
FILLING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: PARMELE, SLEWEN W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-464-148-3
; Sequence 3, Application US/08464148.
; Patent No. 5710026
GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 466 TIGCIGATAAAACTAAAG 483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Best Local Similarity 73.3
Matches 321; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      210 ccardercricardesescalasesas escrices escricias de conservados de 269
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             166 CCATGGTTTTCATGGGGCCAAAGGGAAACACTGCAGGTCAGATGTCTCAGGCACTTTGTT 225
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 286 CAATTAACAGAACTGACACTGAATATGTGCTTAGAACTGCCAACGGGCTCTTTGGAGAAA 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318 AAGTTAACAGAACTGGCACTCAGTACTTGCTTAGAACTGCCAACAGACTCTTTGGAGAAA 377
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Betent No. 5474545

GENERAL INFORMATION:
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES:
CORRESPONDENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STRATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     50 TCATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGCTAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1425;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pry Match 30.4%; Score 214.4; DB 1; Length t Local Similarity 73.3%; Pred. No. 3.8e-55; Ches 321; Conservative 0; Mismatches 101; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                    /product= "CYTOPLASMIC ANTIPROTEINASE-2 PROTEIN"
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TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1425 base pairs
TYPE: NUCLEIC acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        466 TIGCIGATAAACTAAAG 483
TELECOMMUNICATION INFORMATION
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
CCATION: 92..1213
OTHER INFORMATION:
OTHER INFORMATION:
US-08-385-500-1
                                                                                                                                                                                                                                                                                  MOLECULE TYPE: CDNA FEATURE:
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Gaps

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101 GGCCCTGCATGCAAACTCTTTCTAATGCAAGTGGTACTTTTGCCATACGCCTTTTAA 160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    217 CACTITGITITAGIAAAATCGGAGGIGAAGAIGGAGAIATICATCGAGGIITICAGICAC 276
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449 ATGCTGAGCTGAAGGAGCTTTCCTTTATCAGAGCTGCAGAAGAGTCCAGGAAACACATCA 508
                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               101 AAAAGCTAGGGGAAAACAACTCAAACAAC---TTATTTTTTCCCCATGAGCATATCAT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    E: Townsend and Townsend Khourie and Crew Steuart Street Tower, One Market Plaza
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Pred. No. 5.8e-44;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Mismatches 136;
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OTHER INFORMATION: /product= "CYTOPLASMIC"
THER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
US-08-385-500-3
                                                                                                                                              509 ACACCTGGGTCTCAAAAAAGACGGAAG 535
                                                                                  457 ACTCCTGGGTTGCTGATAAACTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PatentIn Release #1.0,
                                                                                                                                                                                                                                                                                                               Sequence 3, Application US/08385500 Patent No. 5712117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              25.1%;
66.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: San Francisco
STATE: California
COUNTRY: US
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1393 base pairs
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Best Local Similarity 66.0
Matches 295; Conservative
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LENGTH: 1393 base pai:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            nucleic acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: CDNA
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NAME/KEY: CDS ·
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic
STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
TELEFAX: (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE:
                                                                                                                                                                                                                                                                                          -08-385-500-3
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                         CYTOPLASMIC ANTIPROTEINASE-2 AND CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES.
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                                                                                                NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
COUNTRY: US
                                                                                                                                                                                                                                                                                                                              COMPART: 02

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: APERICATION DATA:
SOFTWARE: PAECHLIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,148
FILING DATE: 05-UN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-PEB-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 1;
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LOCATION: 12.1239
LOCATION: /product= "CYTOPLASMIC
OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 177.4; DB 1
Pred. No. 5.8e-44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
TELECOMMINICATION INFORMATION:
TELECOMMINICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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TYDE
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Best Local Similarity 66.0%;
Matches 295; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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                                   TITLE OF INVENTION: TITLE OF INVENTION:
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COMPUTER: IBM PC compatible
COMPRATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
FILING DATE: 19911011
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: BENT. SEEDHEN A.
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 29,768
REGISTRATION NUMBER: 16786/157 CHAC
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TELEPHONE: (703)836-9300
TELEFAX: (703)834-9300
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STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: Virginia
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APPLICANT: GOSS, Neil H.
APPLICANT: RICHARDSON, Michael A.
TITLE OF INVENTION: VARIANTS OF PAI-2
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 8
US-07-768-286B-5
: Sequence 5, Application US/07768286B
: Patent No. 5444153
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TYPE: NUCLEIC ACID
STRANDEDNESS: double
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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MOLECULE TYPE:
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                                                       329 TTCTCACTGAAGTGAACAAGGCTGGCACACAGTACCTGCTGAGAAGGGCCAACAGGCTCT 388
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Sprecher, Cindy A.

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES:
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
   TTCTTGTTGCAATTAACAGAACTGACACTGAATATGTGCTTAGAACTGCCAACGGGCTCT
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIN Release #1.0, Version #1.25
SOFTWARE: PAPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FLING DATE: 30-APR-1997
CLASSIFICATION DATA:
APPLICATION NUMBER: 08/385,500
RICHARDATE: 08-FEB-1995
ATOMENY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 25.1%; Score 177.4; DB 1;
Best Local Similarity 66.0%; Pred. No. 5.8e-44;
Matches 295; Conservative 0; Mismatches 136;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LOCATION: 112..1239
OTHER INFORMATION: /product= "CYTOPLASMIC OTHER INFORMATION: ANTIPROTEINASE-3 PROTEIN"
                                                                                                                                                                                                                                                                                                                                                                                           457 ACTCCTGGGTTGCTGATAAACTAAAG 483
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ACACCTGGGTCTCAAAAAAGACCGAAG 535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Guence 3, Application US/08846784
Patent No. 5747645
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 3: SEQUENCE CHARACTERISTICS:
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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linear
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ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                   MOLECULE TYPE:
                                                                                                                                                                                                                                  TISSUE TYPE:
                                                                                                                                  TOPOLOGY:
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US-09-266-910-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             348 TCTTATGATTTCCTCACAGGTTTTACAGATTCCTGTGGCAAATTCTACCAAGCAACGATA 407
                                                                                                                                                                                                                                                                                                                                                                                                                                                 52 ATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGCTAGGG 111
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    81
                                                                                                                                                                                                    /function= "Product binds to
urokinase, tissue plasminogen activator"
/product= "PAI-2 variant, protease sensitive site
                                                                                                                                                                                                                                                                                                             99
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                                                                                                                                                                                                                                                                                         /note= "Codes for human plasminogen activator inhibitor type 2 protein in which amino acids to 98 inclusive have been deleted."
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                                                                                                                                                                                                                                                                                                                                                                                                                    4 ;
                                                                                                                                                                                                                                                                                                                                                                                  Length 1482;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DG/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                Score 103.2; DB 1;
Pred. No. 1.6e-21;
0; Mismatches 198;
                                                                                                                                                                                                                                                                              /evidence= EXPERIMENTAL
                                                                                                                                                                                          experimental
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Patent No. 6344362
GENBLI, INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 53.9%;
Matches 236; Conservative
                                                      Homo sapiens
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
CELL ITYPE: Monocyte
CELL LINE: U937
IMMEDIATE SOURCE:
CLONE: BTA 1922
                                                                                                                                                                          LOCATION: 22..1170 IDENTIFICATION METHOD:
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OTHER INFORMATION:
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                                                                                                                                                          NAME/KEY:
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US-09-266-910-1
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TATTCATCGAGGTTTTCAGTCACTTCTTGTTGCAATTAACAGAACTGACAGGAATATGT 313
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; Sequence 2, Application US/09266910
; Sequence 2, Application US/09266910
; Patent No. 6344362
; GENERAL INFORMATION:
    TITLE OF INVENTION: Use of a recombinant protein as receil TITLE OF INVENTION: hepatitis virus
    NUMBER OF SEQUENCES: 8
; COMPUTER READABLE FORM:
    MEDIUM TYPE: Floppy disk
    COMPUTER: IBM PC compatible
    COMPUTER: IBM PC compatible
    COMPUTER: DATHIN Release #1.0, Version #1.30 (EPO)
    CURRENT APPLICATION DATA:
    APPLICATION NUMBER: US/09/266,910
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 84.8; DB 4;
Pred: No. 5.3e-16;
0; Mismatches 182;
                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Squamous Cell Carcinoma Antigen
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        230 TAAAATCGGAGGTGAAGAT---
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 53.4%;
Matches 251; Conservative
                                                                                INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1245 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                 CELL TYPE: Hepatocyte CELL LINE: HepG2
                                                                                                                                                                                                                                                                                                                                                                                                         Hepatoma
                                                                                                                                                                      TYPE: nucleic acid
STRANDEDNESS: double
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| Patent No. 5783422
| GENERAL INFORMATION:
| APPLICANT: Suminami, Yoshinori
| APPLICANT: Stato, Hiroshi
| APPLICANT: Takeda, Katsumichi
| TITLE OF INVENTION: DAN FRAGMENT CODING FOR SQUAMOUS CELL
| TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN
| VIMBER OF SEQUENCES: 17
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Scully, Scott, Murphy & Presser
                                                                                                                                                                                                                                                                                 Length 1245;
                                                                                                                                                                                                                                                                         Score 84.8; DB 4; Length 1
Pred. No. 5.3e-16;
0; Mismatches 182; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: Scully, Scott, Murphy & Presser CITY: Garden City Plaza STATE: New York COUNTRY: USA
2:
               SEQUENCE CHARACTERISTICS:
LENGTH: 1245 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
TISSUE TYPE: Hepatoma
CELL TYPE: Hepatoma
CELL TYPE: Hepatoma
                                                                                                                                                                                                                                                                         ery Match
st Local Similarity 53.4%;
pches 251; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                   US-09-266-910-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           170
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61 CATGAATTCACTCAGTGAAGCCCAACTTCATTTCGACCTCTTCCAACAGTTCAG 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            170 GGTTTTCATGGGGCAAAGGGAAACACTGCAGCTCAGATGTCTCAGGCACTTTGTTTAG 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 ĠĠrccrcriraĠĠaĠċcaaaĠacaacaĠċrciccaacaĠġrranagaaĠgrrcrircacrrirga 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 TCAAGTCACAGAACACCACAGGAAAAGCTGCAACATATCATGTTGATAGGTCAGGAAA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  301 İGİİCATCACCAĞİTİCAAAAĞCİİCİĞACİĞAAİTCAACAAATÇCACTGAİĞCATATĞA 360
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ------GGAGA 253
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                374 AGATTCCTGTGGCAAATTCTACCAAGCAACGATAAAACAGCTAGACTTTGTGAATGATAC 433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             51 CATGGATGCTCTATCAGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGCTAGG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              254 TATTCATCGAGGTTTTCAGTCACTTCTTGCAATTAACAGAACTGACACAGAATATGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       421 AGATGCCATCAAGAAATTTTACCAGACCAGTGTGGAATCTGTTGATTTTGCAAATGCTCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                37;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 12.0%; Score 84.8; DB 1; Length 1711; Best Local Similarity 53.4%; Pred. No. 6.2e-16; Matches 251; Conservative 0; Mismatches 182; Indels 37
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                                                CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/568,147B
FILING DATE:
CLASSIFICATION DATA:
REPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 80,952
FILING DATE: 02-DEC-1991
ATTONEY/AGENT INFORMATION:
NAME: DIGIGIALO, Frank S.
REGISTRATION NUMBER: 31,346
REGISTRATION NUMBER: 31,346
REFERENCE/POCKET NUMBER: 8425
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
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Patent No. 5370991
GENERAL INFORMATION:
APPLICANT: Remold-O'Donnell, Eileen
IBM PC compatible
NYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: CDNA to mRNA
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TELEX: 230 901 SANS UR
INFORMATION FOR SEQ 1D NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1711 base pairs
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STRANDEDNESS:
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; LOCATION:
US-08-568-147B-1
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 306 GAAACTIGCIAAIAGAITAIAIAGAGAGAAACTIACATITICCIICCIGAGITCIIGGI 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TTCCTGTGGCAAATTCTACCAAGCAACGATAAAACAGCTAGACTTTGTGAATGATACAGA 436
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   tricgacricagadadacardargarccriggccagrigigadrirircagcarigccricida 425
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   18 galacercencescecererescentracecardelescaecionscencidadescentraceces 77
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 77.4; DB 1; Length 1316;
Pred. No. 9.4e-14;
0; Mismatches 211; Indels 16
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                                                          ADDRESSEE: Eilen Remold-O'Donnell, Ph.D. STREET: 197 Clinton Street CITY: Brookline STATE: Massachusetts COUNTRY: United States of America
                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 5.25 inch
COMPUTER: IBM-compatible
OPERATING SYSTEM: MS-DOS Version 3.3
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
FILING DATE: 19910906
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C0279/7012
                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: *...
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/314,383
FILING DATE: 23-FEB-1989
ATTORNEY/AGENT INFORMATION:
NAME: Gates, Edward R.
REGISTRATION NUMBER: 31,616
REFERENCE/DOCKET NUMBER: C0279/;
INFORMATION FOR SEQ ID NO: 12
SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: NUCLEIC ACID
STRANDEDNESS: double standard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 51.4%;
Matches 240; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: genomic DNA HYPOTHETICAL: no
    TITLE OF INVENTION: HUNDMER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ANTI-SENSE:
US-07-755-461A-12
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21 GCAGCTGCGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAATGGCAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 gaagcgrecregecegergregerrrreaceargageagergagereageaaaceceg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78 criceccriegaccrerrecregecerreagreagaacaarccegecregaaacarcricar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1316;
                                                GENERAL INFORMATION:
APPLICANT: Remold-O'Donnell, Eileen
TITLEOF INVENTION: Human Monocyte Elastase Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Wolf, Greenfield & Sacks, P.C.
STREET: 600 Atlantic Ave.
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/315,831A
FILING DATE: September 30, 1994
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
11.0%; Score 77.4; DB 1;
Best Local Similarity 51.4%; Pred. No. 9.4e-14;
Matches 240; Conservative 0; Mismatches 211;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REPERENCE/DOCKET NUMBER: C0279/7016
FELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFRAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LOCATION: 49..1188
OTHER INFORMATION: /codon_start= 49
                                                                                                                                                                                                                                                                                                                                        : Floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
Sequence 12, Application US/08315831A, Patent No. 5663299
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1316 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: mat_peptide
LOCATION: 49..1185
                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: sing
                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
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197 TGCAGCTCAGATGTCTCAGGCACTTTGTTTTAGTAAAATCGGAGGTGAAGATGGAGATAT 256
                                                                                                   81 ATTTGCATTAAACCTTTTGAAAAGCTAGGGGAAAACAACTC----AAACAACTTATTTT 136
                                                                                                                                                                                     137 TITCCCCATGAGCATATCATCAGCCTTGGCCATGGTTTTCATGGGGGAAAGGGAAAGACAC 196
                                                                                                                                                                                                                         138 ctcrcccrrcagcarrrcarcracrargeccargerrrrrcreegaccagadracac 197
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                                                 18 GGAGCGTCCTCGGCGGCTGTTCGCCATGGAGCAGCTGAGCTCAGCAAACACCCG 77
                                                                                                                                                                                                                                                                                                                                                                                                                                                317 IAGAACTGCCAACGGCCTCTTTGGAGAAAGTCTTATGATTTCCTCACAGGTTTTACAGA 376
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                  GCAGCTGCGCGGAGAACTGGGGCTCACCGTCATGGATGCTCTATCAGAAGCAAATGGCAC 80
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT:
TITLE OF INVENTION: Human Monocyte Elastase Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/12509
FILING DATE: herewith
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 30 September 1994
ATTORNEY/AGENT INPORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: C0279/7016
TELECOMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
TELEFAX: 617-720-2441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 12, Application PC/TUS9512509 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: 600 Atlantic Ave.
CITY: Boston.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER PARADABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1316 base pairs
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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MOLECULE TYPE:
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246 TCATTCAAGATTCCAGAGTCTGAATGCTGATATCAACAAACGTGGAGCGTCTTATATTCT 305
                                        317 TAGAACTGCCAACGGGCTCTTTGGAGAAAGTCTTATGATTTCCTCAÇAGGTTTTACAGA 376
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                                                                                                                                                                                                             437 GAAGTCCACAACACGTGTAAACTCCTGGGTTGCTGATAAAACTAAAG 483
                                                                                                                                                                                                                                                      426 AGÁTGCAÁGGAGGCCATAAACCAGTGGGTCAAAGGACAGAGAGA 472
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                                                                                                                                                                                                                                                                                                                                                                                                       ENERAL INFORMATION:
APPLICANT: Remold-O'Donnell, Elleen
TITLE OF INVENTION: Human Monocyte Elastase Inhibitor
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/662,318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADDRESSEE: Wolf, Greenfield & Sacks, p.C. STREET: 600 Atlantic Ave. CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Plumer, Elizabeth R.
REGISTRATION NUMBER: 36,637
REFERENCE/DOCKET NUMBER: C0279/7016
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-720-3500
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1316 base pairs
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OTHER INFORMATION: /codon_start= 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 08/315,831
FILING DATE: September 30, 1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              quence 12, Application US/08662318
bent No. 5827672
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
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ORIGINAL SOURCE:
ORGANISM: Homo sapiens
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PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: nucleic acid
STRANDEDNESS: single
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HYPOTHETICAL:
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; LOCATION:
US-08-662-318-12
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Score 77.4; DB 5; Length 1316;
Pred. No. 9.4e-14;
0; Mismatches 211; Indels 16; Gaps 2;
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                                                                                 FEATURE:
NAME/KEY: CDS
LOCATION: 49..1188
OTHER INFORMATION: /codon_start= 49
FEATURE:
                                                                                                                                                                                                                                                                                                                              Ouery Match
Best Local Similarity 51.4%;
Matches 240; Conservative
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapiens
                                                                                                                                                                                                                ) NAME/KEY: mat_peptide
) LOCATION: 49.1185
PCT-US95-12509-12
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arch completed: May 21, 2003, 19:15:18 time : 57 secs Ч

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RESULT 1
US-09-912-628-4
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Sequence 14, Appl
Sequence 16, Appl
Sequence 16, Appl
Sequence 86, Appl
Sequence 80, Appl
Sequence 3027, Appl
Sequence 21127, Appl
Sequence 21127, Appl
Sequence 1197, Appl
Sequence 1188, Appl
Sequence 1188, Appl
Sequence 1388, Appl
Sequence 288, Appl
Sequence 288, Appl
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Sequence 288, Appl
Sequence 288, Appl
Sequence 1348, Appl
Sequence 288, Appl
Sequence 1348, Appl
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Sequence 188, Appl
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8249.968 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Published Applications NA:*

1: /cgn2_6/ptodata/2/pubpna/USO7_PUBCOMB.seq:*
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GenCore version 5.1.6
(c) 1993 - 2003 Compugen Ltd.
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US-10-116-166-3
US-09-912-628-14
US-10-116-166-12
US-09-912-628-16
US-09-912-628-16
US-09-912-952-86
US-09-928-300-500
US-09-867-701-4671
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US-09-815-343-1348
US-09-922-217-288
US-09-833-263-288
US-08-731-566-1
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                                        OM nucleic - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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Match Length
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US-09-925-301-358	US-09-954-456-1841	US-09-969-347-192	.US-09-998-598-2316	,	US-10-091-442-30	US-09-140-719-30	US-09-796-692-7379	US-10-040-862-7379	US-09-960-352-14649	US-09-735-705-109	US-09-850-716A-109	US-09-897-778-109	US-09-735-705-111	US-09-850-716A-111	US-09-897-778-111	US-09-960-352-7066	US-09-960-352-10531	US-10-012-896-382	US-09-895-793-382	US-09-895-814-382	US-10-010-940-382	US-09-759-143-382	US-09-780-669-382	US-09-822-827-382	US-09-960-352-2546	
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## ALIGNMENTS

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US-09-912-628-4

US-09-912-628-4

Patent No. US2000160491A1

GENERAL HINDOMATION:

APPLICANT: N. det al.

ITILE OF INVENTION: Human Serpin Polymucleotides, Polypeptides, and Antibodies

CURRENT APPLICATION NUMBER: US/09/912,628

CURRENT FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2001-07-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

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(Sequence 3, Application US/10116166
; Sequence 3, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
; PRIOR APPLICATION NUMBER: US/10/116,166
; PRIOR PILING DATE: 2000-08-21
; PRIOR FILING DATE: 2000-08-21
; PRIOR FILING DATE: 1999-03-01
; PRIOR FILING DATE: 1999-03-01
; PRIOR FILING DATE: 1999-03-12
; PRIOR FILING DATE: 1999-03-12
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NAME/KEY: SITE
LOCATION: (635)
OCHER INFORMATION: n equals a,t,g,
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SOFTWARE: PatentIn Ver. 2
SEQ ID NO 3
LENGTH: 706
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APPLICANT: Ni et al.
TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PTOOLP2
CURRENT APPLICATION NUMBER: US/09/912,628
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/02484
PRIOR PILING DATE: 2001-01.28
PRIOR PILING DATE: 2001-01.28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-02-29
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100.0%; Pred. No. 8.5e-219;
tive 0; Mismatches 0;
; LOCATION: (655)
; OTHER INFORMATION: n equals a,t,g, or US-10-116-166-3
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Patent No. US20020160491A1
GENERAL INFORMATION:
                                                                                                                     Query Match
Best Local Similarity 100.
Matches 706; Conservative
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Sequence 16, Application US/09912628
Patent No. US20020160491A1
GENERAL INFORMATION:
APPLICANT: Ni et al.
TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT001P2
CURRENT APPLICATION NUMBER: US/09/912,628
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/02484
PRIOR FILING DATE: 2001-01-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 GAAAACAACTGAAACTAATTTTTTTCCCCCATGAGCATATCATCAGCCTTGGCCATG 120
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                                                                                                                                                                                                                      LOCATION: (585)
CTHER INFORMATION: n equals a,t,g, or US-10-116-166-12
       PRIOR APPLICATION NUMBER: 60/124,094
PRIOR FILING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/149,452
PRIOR FILING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 15
SOGTWARE: PATENTIN Ver. 2.0
SEQ ID NO 12
LENGTH: 599
                                                                                                                                                 TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                     NAME/KEY: SITE
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US-09-912-628-16
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Sequence 12, Application US/10116166

Sequence 12, Application US/10116166

Sequence 12, Application US/10116166

SENERAL INFORMATION:

TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies

TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies

CURRENT APPLICATION NUMBER: US/10/116,166

CURRENT PILING DATE: 2002-04-05

FRIOR APPLICATION NUMBER: PCT/US00/05092

PRIOR FILING DATE: 2000-08-21

PRIOR PILING DATE: 2000-02-29

PRIOR FILING DATE: 1999-03-01
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                                                                                                                                                                                                              Score 586; DB 9; ]
Pred. No. 2.2e-180;
0; Mismatches 0;
                                                                                                                                    LOCATION: (585)
OTHER INFORMATION: n equals a,t,g, or
                                                                                                                                                                                                           Query Match
Best Local Similarity 99.8%;
Matches 598; Conservative (
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 14
                                                                    TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                        NAME/KEY: SITE
                                                                                                                                                           ; OTHER INFORMU
US-09-912-628-14
                                                   LENGTH: 599
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                                                                                                            GAGCCAGGAATCGCCTTCTTCTTACTGCAAAGCCTGCCTTTCACAGGCCCTACTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE REPRENCE: PT001P1
CURRENT APPLICATION NUMBER: US/10/116,166
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/641,721
PRIOR APPLICATION NUMBER: 09/641,721
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-08-21
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
PRIOR FILING DATE: 1999-08-18
SOFTWARE: PATENTIN OFF: 1599-08-18
NUMBER OF SEQ ID NOS: 15
SEQ ID NO 14
FENDAL ARMANIA OFF. 2.0
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OTHER INFORMATION: n equals a,t,g,
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THER INFORMATION: n equals a,t,g,
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ORGANISM: Homo sapiens
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           PRIOR APPLICATION NUMBER: 60/178,769
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/USO0/05082
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 17
SSOFTWARE: Patentin Ver. 2.0
SSOFUN O 16
LENGTH: 608
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US-09-912-628-16
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HER INFORMATION: n equals a,t,g,
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Best Local Similarity 98.4<sup>3</sup>
Matches 598; Conservative
                                                                                                                                                                               ORGANISM: Homo sapiens
                                                                                                                                                                                                                                  LOCATION: (91)
OTHER INFORMATION:
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                                                                                                                                                                                           Length 943;
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| Sequence 500, Application US/09925300
| GENERAL INFORMATION:
| APPLICANT: Craig Rosen, APPLICANT: Steve Ruben | TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies | TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies | FILE REFERENCE: PA10.1 | CURRENT FILING DATE: 2001-08-10 | PRIOR PRING APPLICATION NUMBER: US/09/925,300 | PRIOR PILING DATE: 2000-03-08 | PRIOR FILING DATE: 1999-03-12 | NUMBER OF SEQ ID NOS: 1890 | SEQ ID NOS: 1890 | SEQ ID NOS: 1890 | LENGTH: 1624 | TYPE: DNA
                                                                                                                                                                                                                    Indels
                                                                                                                                                                                       DB 10;
                                                                                                                                                                                    Score 462.8; DB 10;
Pred. No. 4.3e-140;
0; Mismatches 7;
                  CURRENT FILING DATE: 2000-11-30
NUMBER OF SEQ ID NOS: 101
SEQ TONO 86
LENGTH: 943
                                                                                                                                                                                      65.6%;
98.4%;
                                                                                                                                                                           Query Match
Best Local Similarity 98.44
Matches 478; Conservative
                                                                                            ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
; LOCATION: (189) ..(701)
US-09-728-952-86
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APPLICANT: Zhou, Ping
APPLICANT: Zhou, Ping
APPLICANT: Liu, Chenghua
APPLICANT: Mang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Wang, Jian-Rui
APPLICANT: Yanazaki, Vicki
APPLICANT: Yanazaki, Vicki
APPLICANT: Tanazaki, Vicki
APPLICANT: Tanazaki, Vicki
APPLICANT: Ujwal, Manusha L.
APPLICANT: Ujwal, Manusha L.
APPLICANT: Drmanac, Radoje T.
ITILE OF INVENTION: No. US20020111302Alel Nucleic Acids and
TITLE OF INVENTION: Polypeptides
FILE REFERENCE: 799
CURRENT APPLICATION NUMBER: US/09/728,952
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                                                              Query Match
Best Local Similarity 98.4%; Pred. No. 1.9e-177;
Matches 598; Conservative 0; Mismatches 0;
; NAME/KEY: SITE
; JCCATION: (594)
: OTHER INFORMATION: n equals a,t,g, or c
US-10-116-166-14
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Patent No. US20020111302Al
GENERAL INFORMATION:
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184 CCATCATGGATGTTCTCGCAGAAGCAAATGGCACCTTTGCCTTAAACCTTTTGAAAACGC 243
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                                                   107 TAGGGGAAAAÇAÇIÇAAAÇAÇTTATTTTTTÇ-ÇÇÇATGAĞÇATATÇATÇAĞÇTTĞĞ
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| NAME/KEY: misc_feature
| OTHER INFORMATION: Incyte ID No. US20020156263A1 589880CB1
| OTHER INFORMATION: Incyte ID No. US200-974-298-94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 94, Application US/09974298
| Sequence 94, Application US/09974298
| Sequence 96, Application US/09974298
| Sequence 96, Application US/09974298
| GENERAL INFORMATION:
| APPLICANT: Chen, Huei-Mei
| TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER | TITLE OF INVENTION: QENES EXPRESSED IN BREAST CANCER | TITLE OF INVENTION NUMBER: US/09/974,298 | CURRENT FILING DATE: 2001-10-04 | PRIOR PILING DATE: 2000-05-10 | NUMBER OF SEQ ID NUMBER: 60/238,331 | PRIOR FILING DATE: 2000-05-10 | NUMBER OF SEQ ID NO 94 | SEC ID NO 94
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pred. No. 1.8e-58;
0; Mismatches 102;
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Best Local Similarity 73.1%;
Matches 320; Conservative (
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US-09-974-298-94
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US-09-880-107-3027
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: HORMATION:
APPLICANT: Wockley, Joseph G.
APPLICANT: Wockley, Joseph G.
APPLICANT: Scherf, Uwe
APPLICANT: Scherf, Uwe
APPLICANT: Gene Logic, Inc.
APPLICANT: Gene Expression profiles in Liver Cancer
TILE REFERENCE: 44921-5028 W.
CURRENT APPLICATION UNMER: US 60/211,379
PRIOR APPLICATION NUMBER: US 60/211,379
PRIOR PILING DATE: 2000-06-14
PRIOR FILING DATE: 2000-10-02
NUMBER OF SCHOLD NOS: 3950
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 3027
                                                                                                                 Length 1624;
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                                                                                                                      DB 10;
                                                                                                                 Score 251.2; DB 10;
Pred. No. 5.7e-71;
1; Mismatches 119;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 3027, Application US/09880107 Patent No. US20020142981A1 GENERAL INFORMATION:
                                                                                                                            35.6%;
73.6%;
                                                                                                                                 Query Match
Best Local Similarity 73.6
Matches 346; Conservative
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ORGANISM: Homo sapiens
                                                      , ORGANISM: Homo sapiens US-09-925-300-500
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336 AAGTTAACAGAACTGGGACTCAGTACTTGCTTAGAACTGCCAACAGACTCTTTGGAGAA 395
                                                                                                                                      406 TAAAACAGCTAGACTTTGTGAATGATACAGAGAAGTCCACAACACGTGTAAACTCCTGGG 465
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21.6%; Score 152.6; DB 10; Length 456;
Best Local Similarity 67.0%; Pred. No. 3.4e-39;
Matches 254; Conservative 0; Mismatches 109; Indels 16; Gaps
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ORGANISM: Homo sapien
US-09-867-701-4671
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253 ATATTCATCGAGGTTTTCAGTCACTTCTTGTAGCAATTAACAGAACTGACAGAATATG 312
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| Publication No. US20030073144A1
| GENERAL INFORMATION:
| APPLICANT: Benson, Darin R. |
| APPLICANT: Kalos, Michael D. |
| APPLICANT: Lodge, Michael J. |
| APPLICANT: Lodge, Michael J. |
| APPLICANT: Hepler, William T. |
| APPLICANT: Hepler, William T. |
| APPLICANT: Hepler, William T. |
| APPLICANT: Hepler, William T. |
| APPLICANT: Jang, Yuqiu |
| TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: COMPOSITION SAND METHODS FOR THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF CORREST OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF CORREST OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF THE THERAPY |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
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| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF INVENTION: AND DIAGNOSIS OF PANCREATIC CANCER |
| TITLE OF I
Sequence 2112, Application US/09918995
Publication No. US20030073623A1
GENERAL INFORMATION:
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
TITLE OF INVENTION: PROM VARIOUS CDNA LIBRARIES
CURRENT APPLICATION NUMBER: US/09/918,995
CURRENT PILING DATE: 2001-07-30
FRIOR PILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FaetSEQ for Windows Version 3.0
LENGTH: 484
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 21.3%; Score 150.6; DB 9; Length 4 Best Local Similarity 67.0%; Pred. No. 1.6e-38; Matches 235; Conservative 0; Mismatches 104; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; LOCATION: (1)...(484)
; OTHER INFORMATION: n = A,T,C or G
US-09-918-995-2112
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ORGANISM: Homo sapiens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      186 GATGGCCCAGATACTTTCTTTCAATAAAGTGGCGGT---GGTGGAGACATCCACCAGGG 242
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       146 GAGCATATCAGCCTTGGCCATGGTTTTCATGGGGGCAAAGGGAAACACTGCAGCTCA 205
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 126 gagcargriccrgrgcccrgccarggrcracarggggggaaagggaaacacgcrgcaca 185
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                                                                                                                                                                                                                                                                                                                                                      6 GCTCCCGCTCTGGAGTCTGCCATCATGGATGTTCTCGCAGAAGCAAATGGCACCTTGC
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APPLICANT: Carter, Darrick
TLE OF UNUENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
TILE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
FILE REFERENCE: 210121-471C14-471C14-471C14-471C14-471C14-471C14-471C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C14-671C
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14.1%; Score 99.8; DB 9; Length 290;

Best Local Similarity 76.7%; Pred. No. 4e-22;

Matches 122; Conservative 0; Mismatches 77. Tradela
                                                                                                                                               Length 286;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87 ATTAAACCTTTTGAAAAGCTAGGGGAAAACAACTCAAACAACTTATTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        266 ITITICAGICACTICITGITGCAATTAACAGAACTGACACTGAAT 309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       243 chrchdrthchcaccaaghaahcaagchgcacach 286
                                                                                                                                                                                                                                 Indels
                                                                                                                                          Score 142.4; DB 9;
Pred. No. 5.2e-36;
0; Mismatches 71;
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SOFTWARE: FastSEQ for Windows Version 4.0
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Publication No. US20020182191A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Xu, Jiangchun APPLICANT: Lodes, Michael J. APPLICANT: Secrist, Heather APPLICANT: Benson, Darin R. APPLICANT: Masher, Madeleine Joy APPLICANT: Stolk, John A. APPLICANT: Wang, Tongtong
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Skeiky, Yasir A. W.
Fanger, Gary R.
Vedvick Thomas S.
                                                                                                                                                   Query Match 20.2%;
Best Local Similarity 73.6%;
Matches 209; Conservative
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Smith, Carole L.
King, Gordon E.
Wang, Aijun
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US-10-025-380-288
                     ORGANISM: Homo sapiens
US-10-060-036-1797
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TYPE: DNA
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61 aaaaarrchaccaagcagaaaarcaagaagaacrraarchaccaccaragaaaarcca 120
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230 AAAAATTCTACCAAGCAGAGATGGAGGAGCTTGACTTTATCAGCGCCGTAGAGAAGTCCA 171
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Sequence 1188, Application US/09815343

Patent No. US2010055596A1

GENERAL INFORMATION:

APPLICANT: Meacher, Madeleine

APPLICANT: King, Gordon E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND TITLE OF INVENTION: DIAGNOSIS OF COLON CANCER

FILE REFERENCE: 210.121.504

CURRENT APPLICATION NUMBER: US/09/815,343

CURRENT APPLICATION NUMBER: US/09/815,343

CURRENT APPLICATION NUMBER: US/09/815,343

CURRENT APPLICATION NUMBER: US/09/815,343

FILE REFERENCE: 210.101.504

SED ID NOS: 1556

SOFTWARE: PastSEQ for Windows Version 4.0

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                                                                                                                                                                                                                                                 170 gaaaacacaraaacaccrdddradcrdaaaagacagaag 132
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                                                                                                                                                  445 CAACACGTGTAAACTCCTGGGTTGCTGATAAAACTAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May 22, 2003, 00:20:00 Job time : 116 secs
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Best Local Similarity 76.7
Matches 122; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , ORGANISM: Homo sapien
US-09-815-343-1188
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US-09-815-343-1188
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                                                                          May 21, 2003, 13:40:58 ; Search time 1505 Seconds (without alignments) 7597.351 Million cell updates/sec
                                                                                                                                            32308132
GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.
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Maximum Match 100*
Listing first 45 summaries
                                             OM nucleic - nucleic search, using sw model
                                                                                                                                                                                   IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
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em_gss_fun;*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Description SUMMARIES G \* Query Match Length DB Score

BM696260 UI-B-DW0-AW205887 UI-H-BII-BM910133 AGBNCCURT BIG03219 603249869 BI669663 603293204 BG749304 602707953

BM696260 AW205887 BM910193 BI603219 BI669663 BG749304

113 113 123

475.4 404.8 274 253.2 252.6 252.6

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Š. Result

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Clone Distribution: Researchers may obtain clones from Research Genetics (www.resgen.com).
Seg primer: M13 Reverse.
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                                                            /organism="Homo sapiens"
/db xref="taxon:9606"
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                                     Location/Qualifiers
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GENCOURT 6607943 NIH_MGC_98 Homo sapiens cDNA clone IMAGE:5442527
5', mRNA Sequence.
BM910193
BM910193.1 GI:19360572
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Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.G.E. Consortium/LLNL at:
http://image.lln.gov
Rlate: LLCM1918 row: i column: 24
High quality sequence stop: 523.
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/lab_host="BH108 (phage-resistant)"
/note="Organ: brain; Vector: poTB7; Site 1: XhoI; Site 2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI site using the following 5'
adaptor: GGGACGAG(G). Library constructed by Ling Hong
in the laboracory of Gerald M. Rubin (University of
Callfornia, Berkeley) using ZAP-cDNA synthesis kit
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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   Pred. No. 1.5e-78;
0; Mismatches 7; Indels
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/clone_lib="NIH_MGC_98"
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Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.inh.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
CDNA Library Pergaration: Michael J. Brownstein (LLNL)
DNA Sequenching by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenching by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Plate: LiAMIIAG3 row: j column: 18
High quality sequence stop: 787.
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788 bp mRNA linear EST 07-SEP-2001
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11 H MCC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
(Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH MGC Library."
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                                                                                                                                                                                                                                             196 CTGCAGCTCAGATGTCTCAGGCACTTTGTTTTAGTAAAATCGGAGGTGAAGATGGAGATA
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/db xref="taxon:9606"
/clone="IMAGE:5301617"
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96.6%;
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Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
Toshiyuki and Placro Carninci (RIKEN)
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LIML)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC Clone distribution information can be
found through the I.M.A.G.E. Consortium/LINL at:
http://image.llhi.gov
Plate: LLAM11792 row: g column: 01
High quality sequence stop: 659.
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mRNA sequence.
BI669663
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Catarrhini; Hominidae; Homo.
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(NIMH/NHGRI, National this is a NIH_MGC Library."
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                                                                                                                                                                                                                 <u> AGAAGCAAATGGCACCTTTAAACCTTTTGAAAACGCTGGGTAAAGGACAACTCGAA</u>
                                                                                                                                                                                                                                               CAACTTATTTTTTC-CCCATGAGCATATCATCAGCCTTGGCCATGGTTTTCATGGGGGC
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                             GAGCTTCGCTCCTGGGCAGCTGCGGGAGAACTGGGGCTCACCGTCATGGATGCTCTATC
                                                                                                                                                          GAGCCTCGCAGCGGCAGAGAACGGCGACGCGGGCCGGGTCTGCCATCATGGATGTTCTCGC
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                                                                        Length
                             1 others
                                                                        13;
                                                                     Score 253.2; DB 13;
Pred. No. 1.9e-45;
0; Mismatches 124;
constructed by M. Brownstein
Institutes of Health). Note:
175 c 205 g 187 t
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/organism="Homo sapiens"
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Mammalia; Eutheria; Primates;
1 (bases 1 to 664)
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                                                                          35.9%;
                                                                                         Best Local Similarity 73.3
Matches 351; Conservative
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602707953F1 NIH_MGC_43 Homo sapiens CDNA clone IMAGB:4844629 5',
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 804)
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NIH-MGC http://mgc.nci.nih.gov/
NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Enail: cgapbs-r@mail.nih.gov
Tissue Procurement: ATCC
                                                                                                                                                                                                                                                                                                                                                                  6 GAGCTTCGCTCGTGGGCAGCTGCGCGGAAACTGGGGCTCACCGTCATGGATGCTCTATC
                                                                                                                                                                                                                                                                                                                                                                                                   4,
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                                                                                                                                                                                                                                                                                            Score 252.6; DB 13;
Pred. No. 2.7e-45;
0; Mismatches 124;
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/lab_host="DHI08"
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BG749304
BG749304.1 GI:14059957
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Best Local Similarity 73.3%;
Matches 351; Conservative (
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/organisme="Homo sapiens"
/organisme="Homo sapiens"
/organisme="Homo sapiens"
/organisme="Laxon:9606"
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/clone=lib="NIH_MGC_43"
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/lab_host="DH108 (phage=resistant)"
/noce="Organ: eye; Vector: pOTB7; Site_1: XhoI; Site_2: EcoR1; cDNA made by oligo-dT priming. Directionally cloned into EcoR1/XhoI sites using the following 5' adaptor: GGCACAGG(G). Library constructed by Ling Hong in the laboratory of Gerald M. Rubin (University of California, Berkeley) using ZAP-cDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies).
Note: this is a NIH_MGC_Library. |"
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cDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
CNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can h
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov.
Plate: LLCMi682 row: i column: 14
High quality sequence stop: 683.
Location/Qualifiers
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ò 윱 ò 셤 ò g AGENCOURT\_8212433 NIH\_MGC\_112 Homo sapiens cDNA clone IMAGE:6260725 5', mRNA sequence. BG681973 BG681973 GI:21794652 EST.

DEFINITION

RESULT 7 BQ681973

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human.

ACCESSION VERSION KEYWORDS SOURCE

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/ Observations applies.
/ Observations applies.
/ Observations and applies.
/ Clone="IMAGE:6260725"
/ Clone="IMAGE:6260725"
/ Clone="IMAGE:6260725"
/ Clone="IMAGE:111"
/ Lissue type="melanotic melanoma, cell line"
/ Lissue type="melanotic melanoma, cell line"
/ Lissue type="melanotic melanoma, cell line"
/ Lissue type="melanotic melanoma portary"
/ Image="Organ: skin; Vector: portary; site 1: Xhol; Site 2:
ECORI; CDNA made by Oligo-dT priming. Directionally cToned
into ECORI/Xhol sites using the following 5: adaptor:
GGGAGGAG(G). Library constructed by Ling Hong in the
laboratory of Gerald M. Rubin (University of California,
Berkeley) using ZAP-CDNA synthesis kit (Stratagene) and
Superscript II RT (Life Technologies). Note: this is a
NIH MGC Library."
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleogtomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. I (bases 1 to 905)
11 H-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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    - GGTGGAGACATCCACCAGGGCTTCCAGTCTTCTCACCGAAGTGAACAAGACTGGCCAC 341

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Email: cgapbe-rémail.nh.gov
Tissue Procurement: DCTD/DTP
CDNA Library Preparation: Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequenching by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be http://image.llnl.gov
Plate: LLCM2420 row: e column: 14
High quality sequence stop: 649.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAGCTTCGCTCCTGGGCAGCTGCGCGAGAACTGGGGCTCACCGTCATGGATGCTCTATC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AGAAGCAAATGGCACATTTGCATTAAACCTTTTGAAAAAGCTAGGGGAAAACAACTCAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CAACTTATTTTTC-CCCATGAGCATATCATCAGCCTTGGCCATGGTTTTCATGGGGGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            165 GAATGTGTTTTTCTCACCCATGAGCATGTCCTGTGCCTGGCCATGGTCTACATGGGGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Homo sapiens"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 73.3'
Matches 351, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           . . 905
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         261
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Catarrhini; Hominidae; Homo. Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases) 1 to 536)

1 (Dases) 1 to 536)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Contact: Robert Strausberg, Ph.D.

5 Email: cgapbs-r@mail.nih.gov

7 Issue Procurement: AfrCC

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: Incyte Genomics, Inc.

CONA Library Arrayed by: Incyte Genomics, Inc.

CONA Library Arrayed by: Incyte Genomics, Inc.

CONA Library Arrayed by: Colone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llh.gov

Plate: LLAM8444 row: j column: 21

High quality sequence stop: 534.

Location/Qualifiers
                                                                                                                                                                                                                                                                                          BE343971
601070485FI NIH_MGC_12 Homo sapiens CDNA clone IMAGE:3456500 5',
mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    241 CACCGCTGCACATGGCCCAGATACTTTCTTTCATAAAAGTGGCGGT---GGTGGAGA 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      254 TATTCATCGAGGTTTTCAGTCACTTCTTGTTGCAATTAACAGAACTGACACTGAATATGT 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1; Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.4 kb. Library prepared by Life Technologies."
                     TGGCACATTTGCATTAAAACCTTTTGAAAAAGCTAGGGGAAAACAACTCAAACAACTTATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181 TTTCTCACCATGAGCATGTCCTGTGCCCTGGCCATGGTCTACATGGGGGCAAAGGGAAA
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                                                                                                                                                                   439 ACAGAGGAGTCCCGGAAACACATAAACACCTGGGTAGCCCAGAAGACAGAAG 490
                                                                                                          ACAGAGAAGTCCACAACACGTGTAAACTCCTGGGTTGCTGATAAAACTAAAG 483
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Pred. No. 4.7e-45;
0; Mismatches 119; Indels 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo sapiens"
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/clone="Inba" 1456500"
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/tissue_type="cervical carcinoma cell line"
/lab_host="DH10B"
372 ACAGATTCCTGTGGCAAATTCTACCAAGCAACGATAAAACAGCTAGACTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                       BE543971.1 GI:9772616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.6%;
Best Local Similarity 73.8%;
Matches 347; Conservative
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                                                                                                                             432
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                  DEFINITION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                 ACCESSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                          VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                          RESULT 9
BE543971
LOCUS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR PRIMERS
PORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          131
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319 TIGCTCAGAACCGCCAACAGGCTCTTCGGAGAGAGACTTACGGTTTCCTCCCATCTTTC 378
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                                                                        EST 05-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                     Fahrenkrug, S.C., Freking, B.A., Rohrer, G.A., Smith, T.D.L., Casas, E. Stone, R.T., Heaton, M.P., Grosse, W.M., Bennett, G.A., Laegreid, W.W. and Keele, J.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79
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                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 595)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PP DOX 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="taxon:9823"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12 cocrecidacia de cocrecidada de contra contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contra de contr
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 595;
                                                                        BG894979 595 bp mRNA linear 355775 MARC 1PIG Sus scrofa cDNA 5', mRNA sequence. BG894979 GI:14305220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 252; DB 12; Length 5
Pred. No. 3.7e-45;
0; Mismatches 130; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 organism="Sus scrofa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BACKWARD: GTTTTCCCAGTCACGACG
Plate: 120 row: P column: 8
Seg primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                136 g
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Best Local Similarity 72.2%;
Matches 341; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                           pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         157
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ORIGIN
                                                                                                                DEFINITION
ACCESSION
VERSION
                                                                                                                                                                                                        KEYWORDS
SOURCE
ORGANISM
                                                                                                                                                                                                                                                                                                                                                            REFERENCE
AUTHORS
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                            RESULT 8
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/organism="Homo sapiens"
/db_xref="texon:9606"
/clone=lib=NuHMAGE:436604"
/clone=lib=NuHMAGE:436604"
/tissue_type="osteosarcoma, cell line"
/tab_nost="DH103 (phage-resistant)
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Site_2: Sall; Cloned unidirectionally; oligo-dr primed.
Average insert size 1.533 kb. Library enriched for full-length clones and constructed by Life Technologies.
Note: this is a NIH MGC Library."
/d a 216 c 225 g 210 t
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602278558F1 NIH_MGC_86 Homo sapiens cDNA clone IMAGE:4366047 5',
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                                                              395 CATCCACCAGGCTTCCAGTCTCTTCTCCCCGAAGTGAACAAGACTGGCACGCAGTACTT 454
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NIH-MGC http://mgc.ndi.nih.gov/.
                                    194 CACTGCAGCTCAGATGTCTCAGGCACTTTGTTTTAGTAAAATCGGAGGTGAAGATGGAGA
                                                                                                                  254 TATTCATCGAGGTTTTCAGTCACTTCTTGTTGCAATTAACAGAACTGACACTGAATATGT
                                                                                                                                                                                                                           Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
DNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
Found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMIOID frow: d. column: 16
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602940135F1 NIH_MGC_12 Homo sapiens cDNA clone IMAGE:5103344 5',
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Contact: Robert Strausberg, Ph.D.
Contact: Robert Strausberg, Ph.D.
Email: cgapba-r@mail.nin.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
Clone distribution: MGC clone
Figh quality sequence stop: 764.
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clone="ImAGE:10344"

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/lab_hoge="pH108"

/note="Organ: cervix; Vector: pCMV-SPORT6; Site_1: Not1;

Site_2: Sal1; Cloned unidirectionally. Primer: Oligo dT.

Average insert size 1.4 kb. Library prepared by Life
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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National Institutes of Health, Mammalian Gene Collection (MGC)
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BASE COUNT ORIGIN

FEATURES

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AGENICOURT 8744336 Lupski sciatic_nerve Homo sapiens CDNA clone IMAGE:6205988 5', mRNA sequence.
BQ949817.1 GI:22365295
EST.
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NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Conteact: Robert Strausberg, Ph.D.

Email: Gapbs-r@mail.nih.gov

Tissue Procurement: Dr. James R. Lupski
CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:

http://amage.llni.gov

Plate: LLAM18629 row: 1 column: 21

High quality sequence stop: 729.

High quality sequence stop: 729.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Not1; Site_2: Sal1; cDNA made by oligo-dT priming.
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/db_xref="taxon:9606"
/clone="IMAGE:6205988"
/clone lib="Lupski_sciatic_nerve"
/sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           tissue type="sciatic nerve"
|dev stage="adult, 70 yr"
|lab_host="DH10B"
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1 (Dases) 1 to 880;
S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-remail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.llnl.gov
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BM461676.1 GI:18510716
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/lab_host="DH10B (phage-resistant)"
/note="Organ: uterus; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SAll; Cloned unidirectionally. Primer: Oligo dr.
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/organism="Homo sapiens"
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/clone="IMAGE:5533721"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Euteria; Primates; Catarrhini; Hominidae; Homo.
I (bases 1 to 957)
National Institutes of Health, Mammalian Gene Collection (MGC)
National Institutes of Health, Mammalian Gene Collection (MGC)
Contact: Robert Strausberg, Ph.D.
Emali, cgapba-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINL at:
http://image.llnl.gov
                                                                                                                                                        (Baylor
Directionally cloned using the following adaptors:
5'-TCGACCCAGCGTCCG-3' and
5'-TCGACCCAGCGTCCG-3' and
1' S-GACTAGTTCTAGATCGGACGGCCCCCT(15)-3'. Size selected >
1' kb for average insert length 1.87 kb. This is a primary
library, non-amplified. Library constructed by Life
Technologies and donated by J. Lupski, M.D./Ph.D. (Baylor
College of Medicine) and is available through Life
Technologies."
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0; Mismatches 119; Indels
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/organisma"Homo sapiens"
/dx xref="Laxon:9606"
/clone="IMAGE:5181246"
/clone="IMAGE:5181246"
/clone="IMAGE:5181246"
/clone="IMAGE:5181246"
/clone="IMAGE:5181246"
/clone="IMAH MGC_115"
/lab_hofe="MINH MGC_115"
/note="Organ: pooled brain, lung, testis, Vector:
pCMV-SPORT6: Site_1: Not; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (EcoRV site is
oligo-dT primed and directionally cloned (EcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH MGC Library."
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Bukaryota: Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 991)
NIH-MGC http://mgc.nci.nih.gov/.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 251.6; DB 13; Length
Pred. No. 4e-45;
0; Mismatches 119; Indels
         0
         column:
p: 797.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           BQ072385
AGENCOURT 6838712 NIH_MGC_122 Homo
5', mRNA @equence.
Plate: LLAM11952 ....
High quality sequence stop: 7'
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BQ072385.1 GI:19901431
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity 73.8%;
Matches 347; Conservative
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/clohe_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_ins_no_in
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                                                                                                                                     Email: cgapbe-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information con be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Flate: LLAMLSequence stop: 666.
High quality sequence stop: 666.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AGAGAAGTCCAGAAAACACATAAACACCTGGGTAGCTGAAAAGACAGAAG 546
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:5761538"
/clone_lib="NIH" MGC_122"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 35.6
Best Local Similarity 73.8
Matches 347; Conservative
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ORIGIN
                      TITLE
JOURNAL
COMMENT
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Search completed: May 21, 2003, 16:56:59 Job time : 1510 secs

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GenCore version 5.1.4 p5 4578 (c) 1993 - 2003 Compugen Ltd.
                Copyright
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OM protein - protein search, using sw model

May 20, 2003, 10:19:06; Search time 76 Seconds Run on:

(without alignments) 376.959 Million cell updates/sec

US-09-912-628-7 1145 Perfect score:

1 HELRSWAAARRIGAHRHGCS.....SIPKCNSPVTPHGMWXPPSL Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

:peq:

rotal number of hits satisfying chosen parameters: 908470 seqs, 133250620 residues

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Дагараве :

| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1980\_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1981\_DAT:
| SIDS2/gcgdata/geneseq/geneseqp-embl/AA1982\_DAT:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

					SUMMARIES	
Result		Querv				
No.	Score	Match	core Match Length DB ID	DB.	ID	Description
1	1143	8.66	215	. 5	AABOR776	
7	1143		215	200	AA014914	thing acid sequenc
٣	896		199	2 5	AAB08783	Animal Serine proce
4	896	78.3	199	2	AAO14921	Willio acid sequenc
ហ	893		202	2.1	AAB08784	Admin Berine proce
9	893		202	0	AA014922	Hinne acid sequenc
7	885.5		100	15	225577	Human serine prote
α	28.5		100	1 (	/// BOGGA	Amino acid sequenc
o	1		100	7 6	AMOL4 915	Human serine prote
,	000		1/0	23	ABG66743	Human novel nolvne
10	404.5		319	22	AAU02922	Angiotensin conver

	Human prostate can Angiotensin conver Cytoplasmic antipr Human cytoplasmic Novel human secret Cytoplasmic antipr Human cytoplasmic	Psoriastatin type Psoriastatin type Human SCCA2 protei Human aquamous cel SCC antigen. Synt Hepatitis B virus	1 8 8 9 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1	D 0 3 ~ 0 D C
AAU0296 AAU0296 AAU0297 AAB5917 AAB1112	AAB5686 AAU0297 AAR9925 AAY5584 AAY3083 AAR9925 AAR9925	3 AAW15 3 AAW15 3 AAY25 4 AAY72 5 AAY72 6 AAY32 6 AAY32 7 AAY32	0 AAY25928 2 AAY12654 2 AAR12144 1 AAB4367 6 AAR64159 6 AAR64159 2 AAV02233	AAO1492 2 AAO1492 2 AAX1135 2 AAX7266 0 AAY2864 0 AAY2964
200407	204400	0000000	3390 2390 23390 233390 233390 233390 233390 233390 233	4484844
m m m m m m		666 233 666 233 666 233	266 23.2 266 23.2 240 21.0 240 21.0 239 20.9 232 20.3	29 20 20 20 20 20 20 20 20 20 20 20 20 20
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## ALIGNMENTS

AAB08776 standard; Protein; 215 AA (first entry) 02-JAN-2001 AAB08776; 

Amino acid sequence of a human serpin polypeptide.

Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia; cardiavascular disorder; cardiac arrest; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; coular disorder; corneal infection; epithelial cell proliferation; skin aging; sunburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative.

Homo sapiens

Location/Qualifiers Misc-difference

/note= "any L-amino acid which is encoded by TGN" WO200052160-A1 08-SEP-2000

29-FEB-2000; 2000WO-US05082.

99US-0122276. 99US-0124094. 99US-0149452. 01-MAR-1999; 12-MAR-1999; 18-AUG-1999; Misc-difference 211

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Human, serine protease inhibitors; serpin; blood coagulation; proteinase-activated physiological process; gene therapy; antisense therapy; cancer; inflammation; neurological disease;
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                                                                           Claim 12; Page 204; 215pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                     Matches 215; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                immune disease; HMCIS41
                              WPI; 2000-579284/54.
                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                           215 AA;
                  Ruben SM, Ni J;
                                      N-PSDB; AAA64690
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The invention comprises the amino acid and coding sequences of a group of movel human serine protease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and 100 kbm in molecular mass. The majority of serpins function as protease activated physiological processes (e.g. blood coagulation of several proteins on the analy and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present amino acid sequence represents a human serpin protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                          Isolated serine protease inhibitor polypeptide for treating, preventing and/ or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 12; Page 276-277; 288pp; English.
                                    /note= "Encoded by TGN
                  label= Unknown
                                                                                                                                                                                                                                                                              (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                                              28-JAN-2000; 2000US-0178769.
29-FEB-2000; 2000WO-US05082.
                                                                                                                                                                     26-JAN-2001; 2001WO-US02484
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                                                                                                                                                                                                                                                                                                   The present sequence represents a human serpin polypeptide. Serpin is a member of the serine protease inhibitor superfamily of polypeptides. The serpin polymucleotides and polypeptides are used to prevent, treat or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats, corses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. cerebrovascular disorders e.g. cerebrovascular disorders e.g. nervous system disorders, e.g. Alzheimer's disease, infections caused by bacteria, viruses and fungi and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to rangelantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotraxis. The polypeptides can also be used to aid diditive or preservative to increase or decrease storage
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100.0%; Pred. No. 1.3e-118;
iive 0; Mismatches 0;
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                           (HUMA-) HUMAN GENOME SCI INC
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Length 215;
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Score 1143; DB 22;
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                100.0%; Prea. ...
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   99.88;
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AA014921 standard; Protein; 199 AA.

RESULT 4

AA01492

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The present sequence represents a human serpin polypeptide. Serpin is a member of the serine protease inhibitor superfamily of polypeptides. The serpin polymucleotides and polypeptides are used to prevent, treat or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are disgnosed or treated include autorimmum diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplasms of the breast or liver. Cardiovascular ischemia, anglogenesis, nervous system disorders. e.g. cerebral ischemia, anglogenesis, nervous system disorders. e.g. Alzheimer's disease, infections caused by bacteria, viruses and slong and ocular disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial call proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage
Human, serpin, serine protease inhibitor; autoimmune disease; neoplasm; rheumaroid arthritis; hyperproliferative disorder; cerebral ischemia; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimer's disease; infection; occular disorder; sorner infection; epithelial cell proliferation; skin aging; sumburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative.
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                                                                                                                                                                                                                                             /note= "any L-amino acid which is encoded by TGN"
                                                                                                                                                                                          Location/Qualifiers Misc-difference 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 12; Page 13; 215pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       99US-0122276.
99US-0124094.
99US-0149452.
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N-PSDB; AAA74934.
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                                                                                                                                                                                                                                                                                   WO200052160-A1
                                                                                                                                                              Homo sapiens
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18-AUG-1999;
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                                     LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTE 102
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                       Gaps
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                                                                                                                   KIIQTSLSHLEEPGIASSSCYCKACLSQPLIVHSIPKCNSPVTPHGMWXPPSL 215
                                                                                                                                Length 199;
                    2; Indels
 Score 896; DB 21;
Pred. No. 3.5e-91;
0; Mismatches 2;
78.3%;
98.8%;
        Best Local Similarity 98.8
Matches 171; Conservative
 Query Match
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The invention comprises the amino acid and coding sequences of a group of movel human serine processe inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and into kDa in molecular mass. The majority of serpins function as protease activated physiological processes (e.g. blood cosquiation). The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antilesse therapy) and disponsis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present amino acid sequence represents a human serpin protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Isolated serine protease inhibitor polypeptide for treating, preventing and/ or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis
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Best Local Similarity 98.8%; Pred. No. 3.5e-91;
Matches 171; Conservative 0; Mismatches 2; Indels
                                                                    Human serine protease inhibitor (serpin) 1.
                                                                                                                                                                                                                                                                              by TGN'
                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                              /note= "Encoded
                                                                                                                                                                                                                                                            'label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (HUMA-) HUMAN GENOME SCI INC.
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29-FEB-2000; 2000WO-US05082.
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                                  (first entry)
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                                                                                                                                                         immune disease
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                                    19-JUL-2002
                                                                                                                                                                                           Homo sapiens
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 AA014921;
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02-JAN-2001 AAB08784;

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as a food additive or preservative to increase or decrease storage
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                                                                                                   Query Match
Best Local Similarity 93.0
Matches 173; Conservative
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N-PSDB; AAL42748.
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                                                               202 AA;
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                          capabilities.
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C. e.g. Alzheimer's disorders e.g. corneal infection. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to responsate tissues, to transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used
                                                                                                                                                                                                                                                                                                Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia; cardiovascular disorder; cardiac arrest; cerebrovascular disorder; angiogenesis; nervous system disorder; Alzheimar's disease; infection; ocular disorder; corneal infection; epithelial cell proliferation; skin aging; sunburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note= "any L-amino acid which is encoded by NNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   'note= "any L-amino acid which is encoded by NNN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "any L-amino acid which is encoded by TGN"
                                         147 KIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMWXPPSL 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          γď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          encoded
                                                                                                                                                                                                                                                                      Amino acid sequence of a human serpin polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        'note= "any L-amino acid which is
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                  AAB08784 standard; Protein; 202 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99US-0122276.
99US-0124094.
99US-0149452.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     29-FEB-2000; 2000WO-US05082
                                                                                                                                                                                                                                (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 32
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Misc-difference
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12-MAR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-AUG-1999;
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149
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                                                                                                                                                                                                                                                              77 ÓSLLVAINRIDIEYVLRÍANGLEGEKSYDFLIGFIDSCGKFYQATIKQLDFVNDTEKSTT 136
                                      Gaps
                                                                             89
                                                                         34 KARGKQLKQLIFF----PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGF
                                                                                                                                                         90 QSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT
                                                                                                    150 RVNSWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human, serine protease inhibitors; serpin; blood coagulation; proteinase-activated physiological process; gene therapy; antisense therapy; cancer; inflammation; neurological disease;
  Length 202;
                                      Indels
Score 893; DB 21;
Pred. No. 7.7e-91;
2; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ď
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human serine protease inhibitor (serpin)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by TGN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= Unknown
/note= "Encoded
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/note= "Encoded
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/note= "Encoded
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC
      78.0%;
93.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JAN-2001; 2001WO-US02484
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29-FEB-2000; 2000WO-USO5082.
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us-09-912-628-7.rag

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The invention comprises the amino acid and coding sequences of a group of novel human serine procease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and 100 kDa in molecular mass. The majority of serpins function as procease activated physiological processes (e.g. blood coagulation). The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. gene therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The
Isolated serine protease inhibitor polypeptide for treating, preventing and or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                         present amino acid sequence represents a human serpin protein of
                                                                                                                             Claim 12; Page 15; 288pp; English.
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202 AA; Sequence

for diagnosing, treating, preventing and/or prognosing disorders related to the Serpin polypeptides -

99US-0122276. 99US-0124094. 99US-0149452.

29-FEB-2000; 2000WO-US05082

08-SEP-2000

01-MAR-1999; 12-MAR-1999; 18-AUG-1999; (HUMA-) HUMAN GENOME SCI INC

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Ruben SM,

WPI; 2000-579284/54

Claim 12; Page 12; 215pp; English

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                                                                                        QSLLVAINRIDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT 149
                                                                                                      17 KKLGENNSNNLFFSXXXPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGF 76
                                           34 KARGKQLKQLIFF----PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGF
                                                                                                                                     RVNSWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGM
      Length 202;
                          7; Indels
   Score 893; DB 22;
Pred. No. 7.7e-91;
                          Mismatches
                        2,
 78.0%;
93.0%;
        Best Local Similarity 93.0 Matches 173; Conservative
                                                                                                                                                                                   WXPPSL 215
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Query Match
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AAB08777 standard; Protein; 201 AA. 02-JAN-2001 (first entry) AAB08777; AAB08777 

Amino acid sequence of a human serpin polypeptide.

Human; serpin; serine protease inhibitor; autoimmune disease; neoplasm; rheumatoid arthritis; hyperproliferative disorder; cerebral ischemia; cardiovascular disorder; cardiora arrest; cerebrovascular disorder; anglogenesis; nervous system disorder; Alzheimer's disease; infection; ocular disorder; corneal infection; epithelial cell proliferation; skin aging; sunburn; wound healing; organ transplantation; chemotaxis; food additive; food preservative.

Bapiens Homo

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'note= "any L-amino acid"
                                                                 'note= "any L-amino acid"
                                                                                                   'note= "any L-amino
Location/Qualifiers
                                             Misc-difference 33
          Misc-difference
                                                                             Misc-difference
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WO200052160-A1

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The present sequence represents a human serpin polypeptide. Serpin is a member of the serine protease inhibitor superfamily of polypeptides. The serpin polynucleotides and polypeptides are used to prevent, treat or ameliorate a medical conditions in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. Disorders which are diagnosed or treated include autoimmune diseases e.g. rheumatoid arthritis, hyperproliferative disorders e.g. neoplesms of the breast or liver, cardiovascular disorders e.g. cardiac artrest, cerebrovascular disorders e.g. cardiac artrest, cerebrovascular disorders e.g. corneal infection. The polypeptides and fungi and ocular disorders e.g. corneal infection. The polypeptides can consider a skin aging due to subburn, to maintain organs before to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used converted to increase or decrease storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ä
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               210
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KLIGENNSNNLFFSPXXMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 KARGKQLKQLIFFP---MSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQ 90
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    77.3%; Score 885.5; DB 2
93.0%; Pred. No. 5.2e-90;
11ve 2; Mismatches 8
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AAO14915
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ABG66743 standard; Protein; 170

Human novel polypeptide #78.

(first entry)

30-AUG-2002

ABG66743

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The invention comprises the amino acid and coding sequences of a group of novel human serine protease inhibitors (serpins). Serpins are a superfamily of single chain proteins that contain a conserved structure of approximately 370-420 amino acids and generally range between 50 and 100 kDa in molecular mass. The majority of serpins function as protease activated physiological processes (e.g. blood coagulation). The Serpin DNA and amino acid sequences of the invention are useful in the treatment (e.g. green therapy, antisense therapy) and diagnosis of conditions such as cancer, inflammation, neurological diseases and immune diseases. The present amino acid sequence represents a human serpin protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Isolated serine protease inhibitor polypeptide for treating, preventing and/ or prognosing cancers, inflammation, immune disorders and neurological diseases and also for testing and detection e.g. diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      77.3%; Score 885.5; DB 22; Length 201; 93.0%; Pred. No. 5.2e-90;
antisense therapy; cancer; inflammation; neurological disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       . <del>6</del>
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                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Page 14; 288pp; English.
                                                                                                                                                                           label= Unknown
                                                                                                                                                                                                                            /label= Unknown
                                                                                                                                                                                                                                                                          /label= Unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (HUMA-) HUMAN GENOME SCI INC.
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29-FEB-2000; 2000WO-US05082.
                                                                                                                                                                                                                                                                                                                                                                                                                      26-JAN-2001; 2001WO-US02484.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ruben SM, Shi Y;
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                                                                                                                                                                                                                                                        Misc-difference 197
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                                                                                                                                                                                                       Misc-difference 33
                                                                                                                                                    Misc-difference 32
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                                                                                                                                                                                                                                                                                                                             WO200155390-A1
                                      immune disease
                                                                               sapiens
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                                                                                       Homo
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The invention relates to human novel polymucleotides and associated conjugations. The polymucleotides and polymeptides are useful for treating inflammatory conditions such as arthritis, nephritis, Crohn's treating inflammatory conditions such as arthritis, nephritis, Crohn's conditions such as arthritis, nephritis, Crohn's and cancer and for promoting wound healing. The sequences are used to induce the proliferation of neural cells and regeneration of nerve and control intissue, and are useful for the treatment of central and peripheral nervous system diseases and neuropathies, such as Alzheimer's disease, parkinson's disease, Huntington's disease and amyotrophic lateral cell visions. The sequences are involved in chemotactic or chemokinetic activity, regulation of heamatopoieds, treatment of myeloid or lymphoid cell disorders and platelet disorders such as thrombocytopenia, cell resemention of bone, cartilage, tendon, ligament and/or nerve tissue cregeneration of bone, cartilage, tendon, ligament and/or nerve tissue cregeneration of bone, cartilage, tendon, ligament and/or nerve tissue cregeneration or tegeneration and treatment of lung or liver fibrosis, ortocettion or regeneration and treatment of lung or liver fibrosis, repetitision injury in various tissues, immune deficiencies and disorders confidency severe combined immunodeficiency (SCID), bacterial or fungal including severe combined immunodeficiency (SCID), bacterial or fungal inflections, autoimmune disorders egg multiple sclerosis and mysathenia conditions such as asthma, thrombolysis or thrombosis
                                                                                                                                                      cancer, wound healing; central nervous system disease; haematopoiesis; peripheral nervous system disease; amyotrophic lateral sclerosis; tendon; myeloid cell disorder; lymphoid cell disorder; bone; cartilage; ligament; nerve tissue; ulcer; osteoporosis; osteoarthritis; bone degenerative disorder; periodontal disease; reperfusion injury; lung fibrosis; liver fibrosis; autoimmune disorder; bacterial infection; allergic condition; thrombolysis; thrombosis; coagulation disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel nucleic acids and polypeptides for diagnosis, treatment of inflammatory, autoimmune, nervous system, myeloid or lymphoid cell disorders, cancer and promoting wound healing -
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                                                                                                                                                condition; shock; sepsis; immune
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Pred. No. 2.4e-58;
5; Mismatches 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Zhou P,
RT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  novel polypeptides of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Liu C,
Drmanac 1
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83.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-NOV-2001; 2001WO-US47004.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Goodrich RW,
/, Ujwal ML,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-508509/54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                  Human; inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             170 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               HYSE-) HYSEQ INC
                                                                                                                                                                                                                                                                                                              fungal infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; ABK94967
                                                                                                                                                                                                                                                                                                                                                                                    WO200244340-A2
                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Tang YT, Gov
Yamazaki V,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches 120;
                                                                                                                                                                                                                                                                                                                                                                                                                             06-JUN-2002.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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Gaps 90

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abnormality such as deep vein thrombosis.

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The sequence represents an angiotenain converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen P53, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic acids are useful for identification of variant sequences and detection of the invention can be used in the treatment and diagnosis of various discrets including cardiovascular diseases such as arteriosclerosis, myocardial infarction and coronary arterial thrombosis, renal diseases can be an disease such as hypertrophy, immune diseases such as hypertrophy, immune diseases such as hypertrophy, immune diseases such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinese inhibitor IC; wasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                162
                                                                                                                                                           86
27 LFFSPLSISSALAMVFMCAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRIDIE
                                                                                                            103 YVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTKAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiotensin converting enzyme (ACEV) splice variant protein #22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Khosravi R, Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU02922 standard; Protein; 319 AA.
                                                                                                                                                                                                                                                                163 KIIQTSLSHLEEPGIASSSCYCK 185
                                                                                                                                                                                                                                                                                                                                      147 NILLFYFDNILNSFIVSSLQNCQ 169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Fig 22; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17-NOV-2000; 2000WO-IL00766.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99IL-0132978.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-336004/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        N-PSDB; AAS06022.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200136632-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10-DEC-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU02922;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAU0292
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Angiotensin converting enzyme splice variant; ACEV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; dabetic nephropathy; muscular disease; immune disorder; sarcoidosis; nultiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                             93 LVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVN 152
                                                                                                                                                                                                                  Gaрв
                                                                                                                                   92
                                                                                                                                                                  75
                                                                                                                                                  34 KARGKQLKQLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Angiotensin converting enzyme (ACEV) splice variant protein #63
                                                                     Length 319;
                                                                                                  Indels
                                                                                                                                                                                                                                                             153 SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                  :||:||:||:
136 TWVAEKTEG-----KIAELLSPGSVDP------LTRLVLVNAV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Bernstein J;
                                                                 DB 22;
                                                              35.3%; Score 404.5; DB 22;
51.5%; Pred. No. 3.3e-36;
ive 29; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Khosravi R,
                                                                                                                                                                                                                                                                                                                                                                             AAU02963 standard; Protein; 372 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Fig 63; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Azar I,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            .7-NOV-2000; 2000WO-IL00766
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99IL-0133455.
                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (COMP-) COMPUGEN LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                David A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               2001-336004/35.
                                                                               Similarity
                                319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             N-PSDB; AAS06063
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200136632-A2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-DEC-1999;
                                                                                              85;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               25-MAY-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Levine Z,
                                Seguence
                                                                                                                                                                                                                                                                                                                                                                                                              AAU02963;
                                                              Query Match
                                                                                  Local
                                                                                                Matches
                                                                                                                                                                                                                            92
                                                                                                                                                                                                                                                                                                                                             RESULT 11
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acids are useful for identification of variant sequences and detection of candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various disorders including cardiovascular diseases such as arteriosslessench as control and coronary arterial thrombosis, renal diseases such as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as as abbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               93 LVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVN 152
                                                                                                                                                                                                                                                                                                                                                                             92
                                                                                                                                                                                                                                                                                                                                                                                                                    17 KTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTAAQMAQILSFNKSGG-GGDIHQGFQSL 75
                                                                                                                                                                                                                                                                                                                                    Indels 15; Gaps
                                                                                                                                                                                                                                                                                                                                                                             34 KARGKOLKOLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL
                                                                                                                                                                                                                                                                                      35.3%; Score 404.5; DB 22; Length 372; 51.5%; Pred. No. 4.2e-36; ive 29; Mismatches 36; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        153 SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 abnormality such as deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                    Local Similarity
les 85; Conserv
                                                                                                                                                                                                                                                    372 AA;
                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        136
                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                             셤
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granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endochelial cell growth factor; cardiovascular disease; cardiovascular disease; cardiovascular disease; cellular tumour antigen PS3; cyclin-dependent kinase inhibitor IC; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; myocardial infarction; coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidocic pulmonary granulomatous disease; endothelial abnormality;
                                                                                                                                                                                                                               converting enzyme splice variant; ACEV; interleukin 6;
                                                                                                                                                                                  Angiotensin converting enzyme (ACEV) splice variant protein #62.
                                             AAU02962 standard; Protein; 400 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                             vascular disorder; asbestosis
                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                           12-SEP-2001
                                                                                                                                                                                                                                            Angiotensin
                                                                                              AAU02962;
RESULT 12
                         AAU02962
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Novel alternative splicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                             Bernstein J;
                                                                                                                             Khosravi R,
                                                                                                                               Azar I,
                                                          17-NOV-2000; 2000WO-IL00766.
                                                                             99IL-0132978
                                                                                                           COMP-) COMPUGEN LTD.
                                                                                                                               David A,
                                                                                                                                                 WPI; 2001-336004/35.
                                                                                                                                                            N-PSDB; AAS06062.
                    WO200136632-A2
                                                                             17-NOV-1999;
10-DEC-1999;
                                      25-MAY-2001.
                                                                                                                               Levine Z,
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The sequence represents an angiotensin converting enzyme splice variant CC (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor 1C, cellular tumour antigen PS3, and vasoactive intestinal colypeptide receptor 2. The polypeptides and their associated nucleic colypeptide receptor 2. The polypeptides and their associated nucleic condidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various consortable infarction and coronary arterial thrombosis, renal diseases contain infarction and coronary arterial thrombosis, renal diseases uch as diabetic nephropathy, muscular diseases such as hypertrophy, immune disorders such as immune complex nephritis, multiple sclerosis, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   93 LVAINRIDTEYVLRTANGLFGEKSYDFLTGFIDSCGKFYQATIKQLDFVNDTEKSTTRVN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34 KARGKOLKOLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 KTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTAAQMAQILSFNKSGG-GGDIHQGFQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            153 SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           :|||:||:
136 TWVAEKTEG-----KIAELLSPGSVDP-----LTRLVLVNAV 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 404.5; DB 22;
Pred. No. 4.6e-36;
9; Mismatches 36; I
                  Claim 4; Fig 62; 519pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35.3%;
51.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 35.3
Best Local Similarity 51.5
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                     400 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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Angiotensin converting enzyme splice variant; ACBV; interleukin 6; granulocyte colony stimulating factor receptor; glucagon; hypertrophy; platelet-derived endothelial cell growth factor; cardiovascular disease; platelet-derived endothelial cell growth factor; cardiovascular disease; cellular tumour antigen P53; cyclin-dependent kinase inhibitor 1C; vasoactive intestinal polypeptide receptor 2; arteriosclerosis; cancer; mivocardial infarction, coronary arterial thrombosis; renal disease; diabetic nephropathy; muscular disease; immune disorder; sarcoidosis; multiple sclerosis; immune complex nephritis; deep vein thrombosis; nonarcoidotic pulmonary granulomatous disease; endothelial abnormality; vascular disorder; asbestosis. 17-NOV-2000; 2000WO-IL00766. 99IL-0132978. 99IL-0133455. WO200136632-A2. 17-NOV-1999; 10-DEC-1999; Homo sapiens 25-MAY-2001. 

(COMP-) COMPUGEN LTD

Angiotensin converting enzyme (ACEV) splice variant protein #74.

(first entry)

12-SEP-2001

AAU02974 standard; Protein; 204 AA

RESULT 13 AAU02974

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Azar I, Khosravi R,
                                                                                                                                                                                                                                        AAB59176 standard; Protein; 376 AA
                                              Claim 4; Fig 74; 519pp; English.
                                                                                                                                                                                                                                                                                                                                               (HUMA-) · HUMAN GENOME SCI INC
                                                                                                                                                                                                                                                                    Thrombin inhibitor protein.
                                                                                                                                                                                                                                                           22-MAR-2001 (first entry)
                                                                                                                                                          85; Conservative
David A,
         WPI; 2001-336004/35.
                                                                                                                                                     Local Similarity
                                                                                                                                        204 AA;
              N-PSDB; AAS06074
                                                                                                                                                                                                                                                                                                Unidentified
                                                                                                                                                                                                                                                                                                                             22-DEC-1993;
                                                                                                                                                                                                                                                                                                                                      22-DEC-1993;
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                                                                                                                                                                                                                                                                                                                   05-DEC-2000
 Levine Z,
                                                                                                                                       Sequence
                                                                                                                                                 Query Match
                                                                                                                                                                                                                                                   AAB59176;
                                                                                                                                                     Best Loca
Matches
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Thrombin inhibitor; human; thrombolytic; cardiant; cytostatic; nootropic; neuroprotective; antiparkisonian; gene therapy; treatment; carcinoma; cell hypercoaqulation; deep venoue thrombosis; pulmonary embolism; cerebral embolism; thrombic disease; tumor metastases; clot accretion; neurodegenerative disease; Alzheimer's disease; Parkinson's disease.
                                                                                                                Novel polynucleotide encoding thrombin inhibitor polypeptide useful for diagnosis and treatment of diseases related to thrombosis -
                                                                                                                                                                                                                     The present invention relates to a thrombin inhibitor. This is useful for diagnosts and treatment of thrombosis, neurodegenerative diseases such as Alzheimer's disease and Parkinson's disease, tumor metastasis, to prevent proximal extension of deep venous thrombosis or the recurrence of pulmonary embolisms and also to treat risk patients who have congestive heart failure, acute myocardial infarction or cardiomyopathy to prevent the development of deep vein thrombosis or pulmonary embolism. The thrombin inhibitor is also useful for excepting chemical compounds that either up or down regulate its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    93 LVAINRIDIEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34 KARGKQLKQLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ch 35.2%; Score 403.5; DB 22; Length 376; 1 Similarity 51.5%; Pred. No. 5.5e-36; 85; Conservative 29; Mismatches 36; Indels 15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :|||:||:
136 TWVAEKTEG-----KIAELLSPGSVDP-----LTRLVLVNAV 167
                                    Adams MD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Thrombin inhibitor; human; thrombolytic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB11125 standard; Protein; 376 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human thrombin inhibitor protein.
                                  Cao L,
                                                                                                                                                                                Claim 1; Fig 1; 19pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-FEB-2001 (first entry)
                                Fuldner RA,
                                                                         WPI; 2001-060165/07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      376 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-NOV-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  22-DEC-1993;
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                                  Rosen CA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB11125;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 15
AAB11125
ID AAB11
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The sequence represents an angiotensin converting enzyme splice variant (ACEV) polypeptide. The polypeptides of the invention include variants of granulocyte colony stimulating factor receptor, glucagon, interleukin 6, platelet-derived endothelial cell growth factor, cyclin-dependent kinase inhibitor IC, cellular tumour antigen P53, and vasoactive intestinal polypeptide receptor 2. The polypeptides and their associated nucleic candidate compounds capable of binding the molecules. The sequences of the invention can be used in the treatment and diagnosis of various myocardial infarction and coronary arterial thrombosis, renal diseases much as diabetic nephropathy, muscular diseases such as hypertrophy, muscular diseases such as hypertrophy, cancer, sarcoidosis, nonarcoidotic pulmonary granulomatous diseases such as asbestosis and vascular pathologies involving an endothelial abnormality such as deep vein thrombosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             4.
                                                                                           Novel alternative aplicing variants e.g. variant of angiotensin converting enzyme (ACEV), useful in identifying candidate compounds capable of binding to the variant and to detect anti-variant antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVAINRIDIEYVLRTANGLFGEKSYDFLIGFIDSCGKFYQATIKQLDFVNDTEKSTTRVN 152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            76 LTEVNKTGTQYLLRMANRLFGEKSCDFLSSFRDSCQKFYQAEMEELDFISAVEKSRKHIN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       34 KARGKQLKQLIFF-PMSISSALAMVFWGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              75
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thrombin inhibitor; neurodegenerative disease; Alzheimer's;
Pakkinson's; tumour; deep venous thrombosis; pulmonary embolism;
heart.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22; Length 204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35.2%; Score 403.5; DB 22; Length 2
51.5%; Pred. No. 2.2e-36;
tive 29; Mismatches 36; Indels
Bernstein J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
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Adams MD;

Cao L,

Fuldner RA, Rosen CA,

WPI; 2001-006150/01. N-PSDB; AAC65737.

Gaps 92

15;

us-09-912-628-7.rag

New thrombin inhibiting proteins for treating or preventing thrombosis-related diseases, e.g. embolism, tumor metastases, carcinoma, neurodegenerative diseases, e.g. Alzheimer's or Parkinson's

Claim 2; Column 17-20; 19pp; English

cc ints invention describes a novei numan tircumbin initiation will make througholytic, cardiant, cytostatic, nootropic, neuroprotective and antiparkisonian activity and can be used for gene therapy. The thrombin continuous may be used therapetrically or diagnostically to treat or inhibitor may be used therapetrically or diagnostically to treat or continuous thrombosis of the recurrence of pulmonary embolisms and continuous thrombosis of the recurrence of pulmonary embolisms and continuous thrombosis of the recurrence of pulmonary embolisms, to treat high risk patients, e.g. those who have congestive heart failure, acute myocardial infarction or cardiomyopathy to prevent the development of deep vein thrombosis or pulmonary embolism, and as long term therapy for occasional continuous transferin may also be used for treating thrombic disease, tumor metastases, carcinoma of the brain, liver, lung, bone and neoplasmic clotherapets or Parkinson's disease). It can also be used against clotherapets or Parkinson's disease). It can also be used against clother control antibodies. The thrombin inhibitor can be used as producing antibodies. The thrombin inhibitor can be used as pharmaceutical to mammals, such as humans, mice, rats, hamster, dogs, contained the contained of the thrombin inhibitor can be used as the pharmaceutical to man and the contained of the thrombin inhibitor may be used as the thrombin inhibitor may be used as the thrombin inhibitor may be used as the thrombin and antibodies. The thrombin inhibitor can be used as the pharmaceutical to man and the contained and the produces clotheraped the pharmaceutical to man and the pharmaceutical to man and the pharmaceutical to man and the pharmaceutical to man and the pharmaceutical to man and the pharmaceutical thrombin inhibitor may be used as the pharmaceutical thrombin the pharmaceutical thrombin the pharmaceutical thrombin the pharmaceutical thrombin the pharmaceutical thrombin the pharmaceutical thrombin the pharmaceutical thrombin the pharmaceutical thromb This invention describes a novel human thrombin inhibitor which has used as diagnostic probe, for chromosome identification. 8  $\times$  9

376 AA; Sequence

4 Gaps 35.2%; Score 403.5; DB 22; Length 376; ilarity 51.5%; Pred. No. 5.5e-36; Conservative 29; Mismatches 36; Indels 15; Query Match Best Local Similarity 85; Matches

34 KARGKOLKOLIFF-PMSISSALAMVFWGAKGNTAAQMSQALCFSKIGGEDGDIHRGFOSL 92 à g 93 LVAINRIDIEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVN 152 g ò

:|||-||: 136 TWVAEKTEG-----KIABLLSPGSVDP-----LTRLVLVNAV 167 SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197 153

ch completed: May 20, 2003, 10:24:01 ime : 78 secs

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May 20, 2003, 10:22:42 ; Search time 29 Seconds (without alignments) 218.135 Million cell updates/sec
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1 HELRSWAAARRTGAHRHGCS......SIPKCNSPVTPHGMWXPPSL 215
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                      foral number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                       262574 seqs, 29422922 residues
                                                               OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                               US-09-912-628-7
                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                   Scoring table:
                                                                                                                                                                                                                                                                                                       phed:
                                                                                                                                                                                                                  Seguence:
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Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0\* Maximum Match 100\* Listing first 45 summaries

Issued\_Patents\_AA:\*
: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep:\*
!: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep:\*
!: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep:\*
!: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
!: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\*
!: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep:\* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Sequence 2, Sequence 2, Sequence 2, Sequence 2, Sequence 4, Sequence 7, Description Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence Sequence 1 Sequence 1 Sequence 1 Sequence Sequence Sequence Sequence Sequence Sequence US-09-200-965-2 US-08-365-4 148-2 US-08-365-500-2 US-08-846-784-2 US-08-385-500-4 US-08-385-500-4 US-08-365-500-4 US-08-266-910-3 US-09-266-910-3 US-09-266-910-3 US-08-121-714-8 US-08-177-118-8 US-08-177-118-8 US-08-97-040-3 US-09-203-237-3 US-08-121-714-4 US-08-477-108A-4 US-08-477-112-4 PCT-US93-08322-8 US-07-768-286B-6 US-08-487-823B-3 US-08-477-108A-7 -07-768-286B-4 SUMMARIES Query Match Length DB Score Š. 

4

15; Gaps

Length 376; Indele

Query Match 35.2%; Score 403.5; DB 4; Best Local Similarity 51.5%; Pred. No. 4.9e-38; Matches 85; Conservative 29; Mismatches 36;

34 KARGKOLKOLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL 92

à

Sequence 7,

Sequence 7, Appli Sequence 1, Appli Sequence 19, Appli Sequence 19, Appli Sequence 15, Appli Sequence 15, Appli Sequence 112, Appli Sequence 112, Appli Sequence 5, Applii Sequence 5, Applii Sequence 6, Applii Sequence 6, Applii Sequence 7, Applii Sequence 6, Applii Sequence 7, Applii Sequence 6, Applii Sequence 6, Applii Sequence 2, Applii Sequence 2, Applii		
28 223.5 19.5 405 2 US-08-477-112-7 2 2 223.5 19.5 405 5 PCT-US93-08322-7 3 223.5 19.5 415 1 US-09-026-408-4 3 221.5 19.3 415 1 US-07-693-636A-19 3 221.5 19.3 415 1 US-07-693-636A-19 3 221.5 19.3 415 1 US-07-693-636A-19 3 221.5 19.3 434 1 US-07-693-636A-19 3 221.5 19.3 434 1 US-07-679-052A-15 3 221.5 19.2 400 4 US-09-123-912-112 3 219.5 19.2 400 4 US-09-643-597-112 3 200 17.5 406 1 US-08-997-040-5 40 200 17.5 406 2 US-09-203-237-5 41 200 17.5 406 2 US-09-203-237-5 42 200 17.5 406 2 US-09-203-237-5 42 200 17.5 406 2 US-09-203-237-5 42 200 17.5 406 2 US-09-203-237-5 42 200 17.5 406 2 US-09-203-237-5 42 200 17.5 406 2 US-09-203-237-5 42 183.5 16.0 405 1 US-07-899-954-2	ALIGNMENTS	NESULT 1  US-09-200-965-2  Sequence 2, Application US/09200965  Patent No. 6133422  GENERAL INFORMATION:  APPLICANT: ROSEN, ET AL.  ITILE OF INVENTION: Thrombin Inhibitor  NUMBER OF SEQUENCES: 4  CORRESPONDENCE ADDRESS:  ADDRESSEE: CECCHI, STEWART & OLSTEIN  STREET: 6 BECKER PARM ROAD  CITY: NEW JERSEY  COUNTRY: USA  ZIP: 07068  COMPUTER READBLE FORM:  MEDIUM TYPE: 3.5 INCH DISKETTE  COMPUTER: IBM PS/2  OPERATING SYSTEM: MS-DOS  SOFTWARE: WORD PERFECT 5.1  CURRENT MADION NUMBER: US/09/200,965  FILING DATE:  CLASSIFCATION NUMBER: 08/171,817  FILING DATE: 2-DECEMBER 1993  ATTORNEY/AGENT INFORMATION:  PRIOR APPLICATION NUMBER: 35.134  REGISTRATION NUMBER: 36.134  REGISTRATION OFFE SOFT NUMBER: 32500-47  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION INFORMATION:  TELECOMMUNICATION NOTO  STRANDEDNESS:  LENGTH: 376 AMINO ACID  STRANDEDNESS:  TOPOLOGY:  TOPOLO

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linear
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          GENERAL INFORMATION:
APPLICANT: Sprech
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US-08-846-784-2
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ص
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APPLICANT: Sprecher, Cindy A.
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  41 KQLIFFPMSISSALAMVFWGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSILVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26 RNVFFSPMSISSALAMVFMGAKGSTAAQMSQALCLYK----DGDIHRGFQSLLSEVNRTG 81
                                     93 LVAINRIDIEYVLRIANGLFGEKSYDFLIGFIDSCGKFYQATIKQLDFVNDTEKSTIRVN 152
17 KTLGKDNSKNVFFSPMSMSCALAMVYMGAKGNTAAQMAQILSFNKSGG-GGDIHQGFQSL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34; Indels 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    34.3%; Score 392.5; DB 1; Length 374; 52.9%; Pred. No. 9e-37; ive 23; Mismatches 34; Indels 17.
                                                                                                                      SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: DATENTIN BELEASE #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/464,148
PILING DATE: 05-UN-1995
CLASSIFICATION: 435
PRICASIFICATION DATA:
APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-PEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              161 AWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
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; Sequence 2, Application US/08464148
; Patent No. 5710026
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REPRENCE/DOCKET NUMBER: 135
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 34.33
Best Local Similarity 52.93
Matches 83; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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US-08-385-500-2

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Sequence 2, Application US/08846784

Sequence 2, Application US/08846784

Patent No. 5747645

GENERAL INFORMATION:
APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
AFFLICANT: Spreacher, Cindy A.

TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: TOWNSENd and T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 374;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Townsend and Townsend Khourie and Crew
                                                                                                            STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/385,500 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 392.5; DB 1;
Pred. No. 9e-37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 AWKIIOTSLSHLEEPGIASSSCYCKACLSOPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            142 G-----KISEVLDAGTVDP-----LTKLVLVNAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23; Mismatches
                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERRNCE/DOCKET NUMBER: 139
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.3%;
52.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (206) 467-9600
                                                                                                                                                                                                                                                                                  ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Best_Local Similarity 52.9
Matches 83, Conservative
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: San Francisco
STATE: California
COUNTRY: US
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
TELEPAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 376 amino acids
                                                                                                                                                      LENGTH: 376 amino acids
TYPE: amino acids
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-464-148-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : 376 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               / MOLECULE TYPE: protein US-08-385-500-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-08-385-500-4
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Patent No. 5710026

Eatent No. 5710026

Eatent No. 5710026

EAPPLICANT: Sprecher, Cindy A. TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California

CCUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 82 TQYLLRTANRLFGEKTCDFLPDFKEYCQKFYQAELEELSFAEDTEECKKHINDWYAEKTE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
34.3%; Score 392.5; DB 1; Length 374;
Best Local Similarity 52.9%; Pred. No. 9e-37;
Matches 83; Conservative 23; Mismatches 34; Indels 17; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     26 RNVFFSPMSISSALAMVFMGAKGSTAAQMSQALCLYK----DGDIHRGFQSLLSEVNRTG 81
                                OPERATING SYSTEM: PC-DOS/MS-DUS
SOUTHWRE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: PATENTION: CARRENT NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHRARATERISTICS:
LENGTH: 374 amino acids
TYPE: amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC compatible .
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/464,148
FILING DATE: 05-UN-1995
CLASSIPICATION: 435
PRIOR APPLICATION: 435
APPLICATION NUMBER: US 08/385,500
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INPORMATION:
NAME: Parmelee, Steven W.
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    142 G-----KISEVLDAGTVDP------LTKLVLVNAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 161 AWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-846-784-2
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Sequence 4, Application US/08385500
Patent No. 5712117
GENERAL INFORMATION:
CINCY APPLICANT: Sprecher, Cindy A. TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES NUMBER OF SEQUENCES:
ADDRESSEE: Townsend and Townsend Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco STATE: California
                                                                                                                        47 PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                                                                                                                                                                                           107 TANGLEGEKSYDFLTGFTDSCGKFYQATIKOLDFVNDTEKSTTRVNSWVADKT--KAWKI 164
                                                                                                                                                                                                                                                                                    88 TANKLFGEKTCQFLSTFKESCLQFYHAELKELSFIRAAEESRKHINTWVSKKTEGKIEEL 147
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .
9
      DB 1; Length 376;
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Query Match 27.9%; Score 320; DB 1; Length 37. Best Local Similarity 46.3%; Pred. No. 2e-28; Matches 68; Conservative 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
27.9%; Score 320; DB 1; Length 37
Best Local Similarity 46.3%; Pred. No. 2e-28;
Matches 68; Conservative 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: us
ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIIM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: ParentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/385,500
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Parmelee, Steven W.
REFERENCE/DOCKET NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 13952-21
TELECOMMUNICATION INFORMATION:
TELEFOND: (206) 467-960
TELEFOND: (206) 467-960
TELEFOND: (206) 467-960
TELEFOND: (206) 461-961
TELEFOND: (206) 461-961
TELEFOND: (206) 461-961
                                                                                                                                                                                                                                                                                                                                                                                                                 148 LPGSSIDAETRLVLVNAIYFKGKWNEP 174
                                                                                                                                                                                                                                                                                                                                                                    165 IQTSLSHLEEPGIASSSCYCKACLSQP 191
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136
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                                                                                                                                                                                                                                                                                                                                     APPLICANT: Sprecher, Cindy A.
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-2 AND
TITLE OF INVENTION: CYTOPLASMIC ANTIPROTEINASE-3 AND CODING SEQUENCES:
TITLE OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSE: Townsend and Townsend Khourie and Crew
STREEF: Steuart Street Tower, One Market Plaza
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     107 TANGLEGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKT--KAWKI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                        107 TANGLEGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKT--KAWKI 164
                                                                                                    32 PVSISSALAMVLLGAKGNTATQMAQALSLN----TEEDIHRAFQSLLTEVNKAGTQYLLR 87
                        DB 1; Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/846,784
FILING DATE: 30-APR-1997
CLASSIFICATION 1435
PRIOR APPLICATION DATE: 80-APR-1997
FILING DATE: 08-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: PARMATION:
NAME: PARMATION:
NAME: PARMATION:
REGISTRATION NUMBER: 31,990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45;
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46.3%; Pred. No. 2
                                                                                                                                                                                  LPGSSIDAETRLVLVNAIYFKGKWNEP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    IQTSLSHLEEPGIASSSCYCKACLSQP 191
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                                                                                                                                                        165 IQTSLSHLEEPGIASSSCYCKACLSQP 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                     US-08-846-784-4; Sequence 4, Application US/08846784; Patent No. 5747645; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 13
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    : 376 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 46.3<sup>3</sup>
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
US-08-846-784-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    165
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80 GEDGDIHRGFQSLLVAINRIDIEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
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Sequence 2, Application US/08568147B

Fatent No. 5783422

GENERAL INFORMATION:

APPLICANT: Suminami, Yoshinori

APPLICANT: Sekiguchi, Kiyoshi

APPLICANT: Takeda, Katsumichi

TITLE OF INVENTION: DNA FRAGMENT CODING FOR SQUAMOUS CELL

TITLE OF INVENTION: CARCINOMA-ASSOCIATED ANTIGEN

NUMBER OF SEQUENCES: 17

CORRESPONDENCE ADDERSS:

ADDRESSEE: Scully, Scott, Murphy & Presser

STREET: 400 Garden City Plaza

CITY: Garden City

STREET: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 23.2%; Score 266; DB 1; Length 390; Best Local Similarity 37.9%; Pred. No. 3.4e-22; Matches 53; Conservative 28; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 FEKARGKOLKOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DARA:
APPLICATION NUMBER: US/08/568.147B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Use of a recomb
hepatitis virus
                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 11530
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 3, Application US/09266910; Patent No. 6344362; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIPTCATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 800,952
FILING DATE: 02-DEC-1991
ATTORNEY/AGENT INFORMATION:
NAWE: DIGIGILO, FRANK S.
REGISTRATION NUMBER: 31,346
REPRENCE/DOCKET NUMBER: 8425
TELECOMMUNICATION INFORMATION:
TELEPHONE: 516-742-4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              140 FUNDTEKSTTRVNSWVADKT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | | |:| ::||| ::||| :| FANAPEESRKKINSWVESQT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 516-742-4366
TELEFAX: 516-742-4366
TELEX: 230 901 SANS UR
INFORMATION FOR SEQ 1D NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-568-147B-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 9
US-09-266-910-3
                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGEKTYLFLQEYLDAIKKFYQTSVESVD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               47 PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22.4%; Score 257; DB 1; Length 379
46.5%; Pred. No. 3.5e-21;
ive 19; Mismatches 38; Indels
                                                                                                                                                                                    Sequence 8, Application US/08121714
Patent No. 5470970
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TITLE OF SEQUENCES: 8
                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: MS-DOS (Version 5.0)
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATTORNEY/AGENT INCORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; Sequence B, Application US/08477108A; Patent No. 5801001; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                    Richardson
                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardso
STREET: 225 Franklin Street
                                                                                  136 FANAPEESPKKINSWVESQT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             34,819
                                                     140 FVNDTEKSTTRVNSWVADKT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: 00
FELECOMMUNICATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 46.5%
Matches 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Fraser, Janis K. REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                         Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Massachu
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                    US-08-121-714-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 GEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Use of a recombinant protein as receptor of a
                                                                                                                                                                                                                                                                                                                                                                                                                          12;
                                                                                                                                                                                                                                                                                                                                                                          23.0%; Score 263; DB 4; Length 390;
ilarity 37.9%; Pred. No. 7.6e-22;
Conservative 27; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         32 FEKARGKOLKOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   23.0%; Score 263; DB 4; Length 390; 37.9%; Pred. No. 7.6e-22; Live 27; Mismatches 48; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    32 FEKARGKQLKQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG----
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PatentIn Release #1.0, Version #1.30 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Use of a recombi
TITLE OF INVENTION: hepatitis virus
NUMBER OF SEQUENCES: 8
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, 'CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/266,910
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        hepatitis virus
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Patent No. 6344362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             136 FANAPEESPKKINSWVESQT 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 390 amino acids
                                                                                                                                                                                                LENGTH: 390 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                       INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 37.9%
Matches 53; Conservative
                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                        ary Match
est Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                 , ANTI-SENSE: NO
US-09-266-910-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                 53;
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4; Gaps

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Sequence 8, Application PC/TUS9308322
Sequence 8, Application PC/TUS9308322
GENERAL INFORMATION:
APPLICANT: Sager, Ruth
TITLE OF INFORMION: MASPIN, A NOVEL SERPIN WITH TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        47 PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       107 TANGLEGEKSYDFLIGFIDSCGKFYQATIKQLDFVNDTEKSTIRVNSWVADKTK 160
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22.4%; Score 257; DB 2; Length 375;
Best Local Similarity 46.5%; Pred. No. 3.5e-21;
Matches 53; Conservative 19; Mismatches 38; Indels
                                     COUNTRY:
COUNTRY:
COUNTRY:
COUNTRY READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IMP PS/2 Model 50Z or 55SX
COMPUTER: IMP PS/2 Model 50Z or 55SX
COMPUTER: IMP PS/2 Model 50Z or 55SX
COMPUTER: IMP PS/2 Model 50Z or 50SX
COMPUTER: IMP PS/2 Model 50Z or 50SX
COMPUTER: IMP PS/2 Model 50Z or 50SX
COMPUTER: IMP PS/2 Model 50Z
SOFTWARE: WordPerfect (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,112
FILING DATE: 09/01/93
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,236
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
APPLICATION NUMBER: 07/662,216
APPLICATION NUMBER: 07/662,216
APPLICATION NUMBER: 07/662,216
APPLICATION NUMBER: 07/662,216
APPLICATION NUMBER: 07/662,216
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APPLICATION NUMBER: 07/662,216
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APPLICATION NUMBER: 07/662,216
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CITY: Boston
COUNTRY: U.S.A.
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 502 or 558X
OPERATING SYSTEM: Ms-DOS (Version 5.0)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Jamis K.
REGISTRATION NUMBER: 34,819
REFRENCE/DOCKET NUMBER: 0657
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: Fish & Richardson STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCFFILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; TOPOLOGY: linear
US-08-477-112-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
PCT-US93-08322-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
22.4%; Score 257; DB 1; Length 375;
Best Local Similarity 46.5%; Pred. No. 3.5e-21;
cches 53; Conservative 19; Mismatches 38; Indels
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APPLICANT: Zou, Zhiqiang
APPLICANT: Anisowicz, Anthony
ATILE OF INVENTION: MASPIN, A NOVEL SERPIN WITH
TITLE OF INVENTION: TUMOR SUPPRESSING ACTIVITY
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS: 1
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                              CUNTRY: DESCRIBED STATE: MASSACHUSELTS
CUNTRY: U.S.A.
ZII: 02110-2804
COMPUTER: TO S.A.
COMPUTER: TAM PS/2 MOGEL SGZ OF 5SX
COMPUTER: TAM PS/2 MOGEL 5GZ OF 5SX
CORPUTER: TAM PS/2 MOGEL 5GZ OF 5SX
CORPUTER: WORDPERFORM: MS-DOS (Version 5.0)
SOFTWARE: WORDPERFECT (Version 5.1)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: 7, 1995
CLASSIFICATION NUMBER: 08/121,714
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/938,823
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/91
ATTORNEY/AGRIT INFORMATION:
AMANDE TABLE 102/28/91
ATTORNEY/AGRIT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Fraser, Janis K.
REGISTRATION UNMBER: 34,819
REFERENCE/DOCKET NUMBER: 0657
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (617) 542-890
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
US-08-477-108A-8
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                                                                                                                                                                                                                                                                Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
US-08-477-112-8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING STEEN: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/768,286B
FILING DATE: 19911011
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 22.4%; Score 257; DB 5; Best Local Similarity 46.5%; Pred. No. 3.5e-21; Matches 53; Conservative 19; Mismatches 38,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION 1914
PRIOR APPLICATION DATA:
    APPLICATION NUMBER: PCT/AU90/00603
FILING DATE: 20-DEC-1990
ATTORNEY/AGENT INFORMATION:
    NAME: BENT, Stephen A.
    REGISTRATION NUMBER: 29,768
    REFERENCE/DOCKET NUMBER: 16786/157 CHAC
    TELECOMMUNICATION INFORMATION:
    TELEPHONE: (703)836-9300
TELEFAX: (703)693-4109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6. Application US/07768286B
Patent No. 5444153
GENERAL INFORMATION:
APPLICANT: GOSS, Neil H.
APPLICANT: RICHARDSON, Michael A.
TITLE OF INVENTION: VARIANTS OF PAI-2
CORRESPONDENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
                                                                                                                                                                                                        00530/072001
PRIOR APPLICATION NUMBER: 07/938,823
FILING DATE: 09/01/92
APPLICATION NUMBER: 07/844,296
FILING DATE: 02/28/92
APPLICATION NUMBER: 07/662,216
FILING DATE: 02/28/91
ATORNEY/AGENT INFORMATION:
NAME: Fraser, Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 00530//
TELEPHONE: (617) 542-8906
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                         IELEX: 200154
INPORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 899149
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
PCT-US93-08322-8
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: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 15
US-07-768-286B-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE:
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95 AINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSW 154
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                                                                                                                                               ô
                                                                                                            Length 382;
                                                                                                         21.5%; Score 246; DB 1; Length 38
38.9%; Pred. No. 6.6e-20;
iive 27; Mismatches 50; Indels
                                                                                                                                                                                                                                                                                                                                                                           Search completed: May 20, 2003, 10:27:21
Job time : 32 secs
             LENGTH: 382 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-768-286B-6
                                                                                                      Query Match
Best Local Similarity 38.9%
Matches 49; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                               155 VADKTK 160
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May 20, 2003, 10:26:02 ; Search time 56 Seconds (without alignments) 380.752 Million cell updates/sec
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1 HELRSWAAARRIGAHRHGCS.....SIPKCNSPVTPHGMWXPPSL 215
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
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Gapop 10.0 , Gapext 0.5
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Perfect score:
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1 number of hits satisfying chosen parameters: 375593 seqs, 99172665 residues Minimum DB seq length: 0 Maximum DB seq length: 200000000

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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries **Database** :

cgn2\_6/ptodata/1/pubpaa/US08\_PUBCOMB.pep:\*
cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep:\*
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/cgn2\_6/ptodata/1/pubpaa/US0\_NEW\_PUB.pep:\* Published Applications AA:\*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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14	229	20.0	41	6	US-10-116-166-11	
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4	222	19.4	42	σ	US-09-912-628-11	Sequence 11, Appl

Sequence 9, Appli Sequence 112, App Sequence 112, App Sequence 112, App	Sequence 10, Appl Sequence 8, Appl Sequence 947, App Sequence 947, App Sequence 12, Appl Sequence 10, Appl	994444	Sequence 34, Appl Sequence 4, Appli Sequence 58, Appl Sequence 27, Appl Sequence 27, Appl Sequence 27, Appl	92, 8, 7,
9 US-10-116-166-9 10 US-09-735-705-112 10 US-09-850-716A-112 10 US-09-897-778-112	9 US-09-912-628-10 9 US-10-116-166-8 9 US-10-012-896-947 9 US-09-895-814-947 9 US-09-912-628-12 9 US-10-116-166-10	9 US-10-012-096-946 9 US-09-995-914-946 9 US-10-22-857-4 9 US-11-135-629-1 9 US-10-091-442-34	10 US-09-140-719-34 1 US-08-731-566-4 10 US-09-755-665-58 9 US-10-165-605A-27 10 US-09-910-430-27 9 US-09-924-340-92	9 US-09-992-600A-92 9 US-10-000-489-92 9 US-09-993-180-6 9 US-10-025-514-2
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Squence 7, Application US/09912628

Squence 7, Application US/09912628

Patent No. US20020160491A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: Human Serpin Polynuclectides, Polypeptides, and Antibodies

FILE REFERENCE: PT001P2

CURRENT APPLICATION NUMBER: US/09/912,628

CURRENT FILING DATE: 2001-07-26

PRIOR PELING DATE: 2001-07-26

PRIOR PILING DATE: 2001-01-26

PRIOR PILING DATE: 2000-01-28

PRIOR PILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

NUMBER OF SEQ ID NOS: 17

SOFTHARE: PATENTING DATE: 2000-02-29
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-912-628-7
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US-09-912-628-7
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Gape ö Length 215; 0; Indels 99.8%; Score 1143; DB 9; L 100.0%; Pred. No. 5.7e-114; ive 0; Mismatches 0; Matches 215; Conservative Query Match Best Local Similarity

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61 AKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFL 120 61 AKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFL 120 1 HELRSWAAARRIGAHRHGCSIRSKWHICIKPFEKARGKQLKQLIFFPMSISSALAMVFWG 60 1 HELRSWAAARRTGAHRHGCSIRSKWHICIKPPEKARGKQLKQLIFFPMSISSALAMVFMG 60 q ò g ò

TGFTDSCGKPYQATIKQLDPVNDTEKSTTRVNSWVADKTKAWKIIQTSLSHLEEPGIASS 180 121

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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-10-116-166-13
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
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Pred. No. 1.2e-87;
0; Mismatches 2.
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Pred. No. 1.2e-87;
0; Mismatches 2.
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CURRENT APPLICATION NUMBER: US/10/116,166
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/641,721
PRIOR APPLICATION NUMBER: PCT/US00/05092
PRIOR FILING DATE: 2000-02-29
PRIOR APPLICATION NUMBER: 60/122,276
PRIOR APPLICATION NUMBER: 60/122,276
PRIOR FILING DATE: 1999-03-01
PRIOR PLING DATE: 1999-03-01
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
                              PCT/US00/05082
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, Sequence 13, Application US/10116166
; Publication No. US20030040097A1
; GENERAL INFORMATION:
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: PCT/U;
PRIOR FILING DATE: 2000-02-29
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 15
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Best Local Similarity 98.8%;
Matches 171; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Homo sapiens
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Best Local Similarity
Matches 171; Conserv
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LOCATION: (195)
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TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies FILE REFERENCE: PT001P2
CURRENT APPLICATION NUMBER: US/09/912,628
CURRENT FILING DATE: 2001-07-26
PRIOR APPLICATION NUMBER: PCT/US01/02484
PRIOR FILING DATE: 2001-01-26
PRIOR APPLICATION NUMBER: 60/178,769
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OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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           121 TGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTKAWKIIQTSLSHLEEPGIASS 180
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Pred. No. 5.7e-114;
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100.0%; Pred. No. 5...
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                                                                                                                 181 SCYCKACLSOPLLVHSIPKCNSPVTPHGMWXPPSL 215
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CURRENT APPLICATION NUMBER: US/10/116,166
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 09/641,721
PRIOR PELLING DATE: 2000-08-21
PRIOR PELLING DATE: 2000-02-29
FILING PAPE: 2000-02-29
FILING PAPE: 1999-03-01
PRIOR FILING DATE: 1999-03-01
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR PELLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR PELLING DATE: 1999-03-12
PRIOR PELLING DATE: 1999-03-12
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Patent No. US20020160491A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                   Sequence 5, Application US/10116166 Publication No. US20030040097A1 GENERAL INFORMATION:
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TITLE OF INVENTION: SER
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Matches 215;
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SOFTWARE: Patentin Ver. 2.0
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                                                                                                                                                                                                     Sequence 17, Application US/09912628
| Patent No. US20020160491A1 |
| GENERAL INFORMATION: |
| GENERAL INFORMATION: |
| TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies |
| FILE REFERENCE: PT001P2 |
| TITLE OF INVENTION: HUMBER: US/09/912,628 |
| CURRENT APPLICATION NUMBER: PCT/US01/02484 |
| CURRENT FILING DATE: 2001-01-26 |
| PRIOR FILING DATE: 2000-01-28 |
| PRIOR FILING DATE: 2000-01-28 |
| PRIOR FILING DATE: 2000-01-28 |
| PRIOR FILING DATE: 2000-01-28 |
| PRIOR FILING DATE: 2000-01-28 |
| PRIOR FILING DATE: 2000-01-29 |
| NUMBER OF SEQ ID NOS: 17 |
| SOFTWARE: PATENTIN Ver. 2.0
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; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids US-09-912-628-17
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OTHER INFORMATION: Xea equals any of the naturally occurring L-amino acids
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Publication No. US20030040097A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Serpin Polynucleotides, Polypeptides, and Antibodies
OSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTT 149
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                                                                                        147 KIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMWXPPSL 199
                                                              163 KIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMWXPPSL
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78.0%; Score 893; DB 9; Length 202;
9t Local Similarity 93.0%; Pred. No. 2.5e-87;
Ches 173; Conservative 2; Mismatches 7; Indels
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ORGANISM: Homo sapiens
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LOCATION: (31)
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LOCATION: (32)
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US-09-912-628-17
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Sequence 8, Application US/09912628

Patent No. US20020160491A1

GENERAL INPORMATION:

APPLICAMY: Ni et al.

TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies

FILE REFERENCE: PT001P2.

CURRENT APPLICATION NUMBER: US/09/912,628

CURRENT FILING DATE: 2001-07-26

PRIOR PELING DATE: 2001-01-26

PRIOR PLING DATE: 2001-01-26

PRIOR PLING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-29

PRIOR FILING DATE: 2000-01-29

NUMBER OF SEQ ID NOS: 17
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CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: US/10/116,166
PRIOR APPLICATION NUMBER: 09/641,721
PRIOR PILING DATE: 2000-08-21
PRIOR PLING DATE: 2000-02-29
PRIOR PLING DATE: 2000-02-29
PRIOR PLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR PLING DATE: 1999-03-12
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR FILING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-03-12
PRIOR PLING DATE: 1999-08-18
NUMBER OF SEQ ID NOS: 15
SOFTWARE: PATENTIN VET: 2.0
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ORGANISM: Homo sapiens
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LOCATION: (33)
OTHER INFORMATION:
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OTHER INFORMATION:
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SEQ ID NO 1440
US-10-116-166-6
                                                      Query Match
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LOCATION: (197)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
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Pred. No. 1.6e-86;
2; Mismatches 8;
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Publication No. US20030040097A1
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Best Local Similarity 93.0%;
Matches 172; Conservative 5
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OTHER INFORMATION: Xaa evamme/KEY: SITE
LOCATION: (33)
OTHER INFORMATION: Xaa evammer.
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CTHER INFORMATION: Xaa
NAME/KEY: SITE
                                                                                                                                                                                                                                                                            LOCATION: (33)
OTHER INFORMATION: Xaa
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                                                                      TYPE: PRT
ORGANISM: Homo sapiens
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XPPSL 201
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NAME/KEY: SITE
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US-10-116-166-6
            SEQ ID NO 8
LENGTH: 201
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LVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVN 152
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                                                                                                                                                                                                                                                                                    210
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                                          Gaps
                                                                                       34 KARGKQLKQLIPFP---MSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQ 90
                                                                                                                                     17 KKLGENNSNNLFFSPXXMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQ 76
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        34 KARGKOLKOLIFF-PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFOSL
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Length 201;
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TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PAIOL
CURRENT APPLICATION NUMBER: US/09/925,300
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: CT/US00/05988
PRIOR FILING DATE: 2000-03-08
PRIOR FILING DATE: 2090-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
PRIOR FILING DATE: 1999-03-12
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                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
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TWVAEKTEG-----KIAELLSPGSVDP------LTRLVLVNAV 250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 US-09-974-298-95
Sequence 95, Application US/09974298
Sequence 95, Application US/09974298
Sequence 95, Application US/09974298
SEREMEN IN-US/0020156263A1
GENERAL INFORMATION:
TITLE OF INVENTION: GENES EXPRESSED IN BREAST CANCER
FILLE REPERENCE: PA-0037 P
CURRENT APPLICATION NUMBER: US/09/974,298
CURRENT FILING DATE: 2001-10-04
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Best Local Similarity 51.5%; Pred. No. 1.3e-34;
Matches 85; Conservative 29; Mismatches 36
Score 885.5; DB 9
Pred. No. 1.6e-86;
                                               2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 9
US-09-925-300-1440
US-09-925-300-1440
; Sequence 1440, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
77.3%;
ilarity 93.0%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: PRT
CRGANISM: Homo sapiens
US-09-925-300-1440
                      Best Local Similarity
Matches 172; Conserv
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-301-1200
                                             Query Match
Best Local Similarity
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Best Local Similarity
Matches 49; Conserv
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US-09-925-301-1200
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US-09-912-628-13
         US-08-731-566-2
                                                                                Matches
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                                                                                                                                                                                                                                                                                                            41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                  26 RNVFFSPMSISSALAMVFMGAKGSTAAQMSQALCLYK----DGDIHRGFQSLLSEVNRTG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENES FROM PSORIATIC EPIDERMIS:
TIN TYPE I AND PSORIASTATIN TYPE II
                                                                                                                                                                                                                                                                               17;
                                                                                                                                                                                                                                            Length 374;
                                                                                                                                                                                                                                                                          23; Mismatches 34; Indels
                                                                                                                                                             NAME/KEY: misc feature
; OTHER INFORMATION: Incyte ID No. US20020156263A1 589880CD1
US-09-974-298-95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 02109-1775

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
APPLICATION NUMBER: US/08/731,566
                                                                                                                                                                                                                                          34.3%; Score 392.5; DB 9; 52.9%; Pred. No. 1.5e-33;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             142 G-----KISEVLDAGTVDP-----LTKLVLVNAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                        161 AWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 11
US-08-731-566-2
Sequence 2, Application US/08731566
Sequence 2, Application US/08731566
Publication No. US20030072752A1
GENERAL INFORMATION:
TITLE OF INVENTION: TWO NOVEL GENES FROM
TITLE OF INVENTION: PSORIASTATIN TYPE I NOWBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/731,566
FILING DATE: 16-0CT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/013,755
FILING DATE: 20-MAR-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/005,679
FILING DATE: 17-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: 28 State Street
CITY: Boston
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REGISTRATION NUMBER: 35,965
REFERENCE, DOCKET NUMBER: MGI
TELECOMMUNICATION INFORMATION:
PRIOR APPLICATION NUMBER: 60/23:
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 194
SOFTWARE: PERL Program
SEQ ID NO 95
LENGTH: 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (617) 227-7400
                                                                                                                                                                                                                                  Query Match
Best Local Similarity 52.99
Matches 83; Conservative
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                               ORGANISM: Homo sapiens
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                                                                                                              TYPE: PRT
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Sequence 13, Application US/09912628

Sequence 13, Application US/09912628

Patent No. US20020160491A1

GENERAL INFORMATION:

APPLICANT: Ni et al.

TITLE OF INVENTION: Human Serpin Polynucleotides, Polypeptides, and Antibodies

FILE REFERENCE: PT001P2

CURRENT APPLICATION NUMBER: US/09/912,628

CURRENT FILING DATE: 2001-01-26

PRIOR APPLICATION NUMBER: 60/178,769

PRIOR APPLICATION NUMBER: 60/178,769

PRIOR PILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-01-28

PRIOR FILING DATE: 2000-02-29

NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUMBER: PALENT NUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             90 PFSISSAMAMVFLGTRGNTAAQLSKTFHFNTV----EEVHSRFQSLNADINKRGASYILK 145
                                                                                                                                                                                                                                                  32 FEKARGKOLKOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG------ 79
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Sequence 1200, Application US/09925301

GENERAL INFORMATION:

TITLE OF INVENTION:

TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies

FILE REPRENCE: PA106

CURRENT APPLICATION NUMBER: US/09/925,301

CURRENT FILING DATE: 2001-08-10

PRIOR APPLICATION NUMBER: PCT/USO0/05882

PRIOR APPLICATION NUMBER: PCT/USO0/05882

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 1694

SEQ ID NOS: 1694

SEQ ID NOS: 1694
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24.3%; Score 278; DB 1; Length 390; 39.3%; Pred. No. 2.5e-21; Live 27; Mismatches 46; Indels
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k; Pred. No. 3.4e-17;
23; Mismatches 38;
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NUMBER SOFTWARE: FAST
SOFTWARE: FAST
SEQ ID NO 110
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SEPTIAL INFORMATION:
TITLE OF INVENTION Serpin Polymucleotides, Polypeptides, and Antibodies
FILE REPERENCE: PT001P1
CURRENT APPLICATION NUMBER: US/10/116,166
CURRENT FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: PCF/US00/05092
PRIOR FILING DATE: 2000-08-21
PRIOR APPLICATION NUMBER: PCF/US00/05092
PRIOR APPLICATION NUMBER: 60/12,276
PRIOR APPLICATION NUMBER: 60/12,276
PRIOR APPLICATION NUMBER: 60/12,276
PRIOR APPLICATION NUMBER: 60/124,094
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-12
PRIOR PILING DATE: 1999-03-18
NUMBER OF SEQ ID NOS: 15
NUMBER OF SEQ ID NOS: 15
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COCATION: (37)
OTHER INNERWATION: Xaa equals any of the naturally occurring L-amino acids
10-116-166-11
                                                                         ; LOCATION: (37)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-912-628-13
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                                                                                                                                                                             Query Match
20.0%; Score 229; DB 9; Length 41;
Best Local Similarity 100.0%; Pred. No. 2e-17;
Matches 41; Conservative 0; Mismatches 0; Indels
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Patent No. US20020052329A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                              quence 11, Application US/10116166
Nication No. US20030040097A1
NERAL INFORMATION:
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Fan, Lidun
Kalos, Michael D.
Bangur, Chaitanya S.
Hosken, Nancy
Fanger, Gary R.
Li, Samuel X.
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               TYPE: PRT
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Homo sapiens
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Best Local Similarity
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US-09-735-705-110
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LENGTH: 41
LENGTH: 41
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APPLICANT:
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APPLICANT:
APPLICANT:
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APPLICANT:
APPLICANT:
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                                                            FEATURE:
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85 ----IHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
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                                                                                                                                                                                                                                                                                                                                                Length 391;
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Exanger, Neil
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REPERENCE: 210121.455C14
CURRENT APPLICATION NUMBER: US(99/735,705
CURRENT FILING DATE: 2000-12-12
NUMBER OF SEQ ID NOS: 419
                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ---NEKIKDLFPDGSISSS 172
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 FVNDTEKSTIRVNSWVADKTKAWKIIQTSLSHLEEPGIASSS 181
                                                                                                                                                                                                                                                                                                                                                ; Score 224; DB 10;
; Pred. No. 1.5e-15;
31; Mismatches 54;
                                                                                                                                                                                                                                                                                                                                                                                                                                       38 KOLKO----LIFFPMSISSALAMVFMGAKGNTAAOMSOAL--
                                                                                                                                                                                               FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Search completed: May 20, 2003, 10:35:38 Job time: 57 secs
                                                                                                                                                                                                                                                                                                                                                  ch
1 Similarity 32.7%;
53; Conservative 31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ||| ::| ::|||
137 FVNAADESRKKINSWVESKT-
                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Homo sapien
US-09-735-705-110
                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 53; Conserval
```

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GenCore version 5.1.4 p5_4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
```

- protein search, using sw model OM protein Run on:

May 20, 2003, 10:22:17 ; Search time 44 Seconds (without alignments) 469.748 Million cell updates/sec

US-09-912-628-7 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

283224 seqs, 96134422 residues ched:

Total number of hits satisfying chosen parameters:

283224

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

pir 73:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	cript	placental thrombin		0.01		leupin precursor -	squamous cell carc	ela		elastase inhibitor	headpin serine pro	•		bomapin - himan	plasminogen activa	ovalbumin-related	alpha-1 proteinase	alpha-1-antitrypsi	alpha-1 proteinase	alpha-1 proteinase	contrapsin-related	alpha-1 proteinage		4	alpha-1-antiprotei	alpha-1-antiprotei	Contransin predicts	intracellilar con	conticosteroid-bin	alpha 1-proteinase	
SUMMARIES	ID	A48681	A59273	A57488	B59273	138202	138201	A42421	S38962	527383	JC7118	A32853	520047	139184	\$19896	DYCH	149471	149452	4	149474	823675	149470	149472	JH0494	A39088	JX0346	JX0129	A53120	A28321	156481	
	DB	-	7	N	ď	N	ď	N	N	N	~	~	~	~	~		~	7	7	N	N	~	N	~	~	~	~	~	7	~	
	Query Match Length	376	374	378	376	390	390	379	378	379	391	415	415	397	416	388	402	413	413	413	418	413	413	418	405	406	418	418	405	413	
*	Ouery Match	35.3	34.3				23.5					19.3		18.6		17.3							16.3				16.1		16.0	16.0	
	Score	2	392.5	2	320	272	266	∾	255.5	240	224	221.5	216.5	213.5	213	198.5	191.5	190.5	190.5	189.5	188.5	186.5	186.5	186.5	œ	.185	184.5	æ	183.5		
	Result No.	-	7		4.⁻	ហ	9	7	80	σ	10	11	12	13	14	15	16	11	18	19	90	21	22	23	24	25	56	27	28	50	

contrapsin precure	alpha-1-antiprotei	alpha-1-antitrypsi	kallikrein-binding	alpha-1-antitrvpsi	alpha-1-antitrypsi	corticosteroid-bin	alpha-1-antitrypsi	alpha-1-antitrypsi	alpha-1-antiprotei	alpha-1-antiprotei	serine proteinase	estrogen-regulated	alpha-1-antiprotei	serine proteinase	alpha-1-antitrypsi
C39088	839088	ITRT	S19724	S21097	A54968	A36117	ITBA	ITSH	JX0267	S54981	\$11320	A42440	JX0154	831507	ITHU
~ 0	7	-	~	~	7	~	-	-	7	~	7	~	~	-	7
410	388	411	417	416	413	383	409	416	413	413	408	436	413	418	418
16.0	15.9	15.9	15.9	15.8	15.6	15.6	15.3	15.3	15.2	15.2	15.2	15.2	15.1	14.9	14.8
183	787	181.5	181.5	181	179	178.5	175	175	174	174	173.5	173.5	173	170.5	169
0.5	Ţ :	32	23	4	ຼຸ	9	37	8	39	40	ᅼ	2	Ω.	44	ທູ

## ALIGNMENTS

RESULT 1 A48681 placental thrombin inhibitor - human

_	N. A. Transfer and Control of the co
	N'ALLEINACE NAMES: CYCOPIASMIC ANTIDIOTEINASE; INTRACELLULAR SERINE PROTEINASE INDIDITOR
	C;Species: Homo sapiens (man)
	C;Date: 07-Apr-1994 #sequence_revision 07-Jul-1995 #text_change 18-Jun-1999
	C;Accession: A48681; A54352; A46672; B46672; C46672; S35750
	R;Coughlin, P.; Sun, J.; Cerruti, L.; Salem, H.H.; Bird, P.
	Proc. Natl. Acad. Sci. U.S.A. 90, 9417-9421, 1993
	A, Title: Cloning and molecular characterization of a human intracellular serine protein.
	A; Reference number: A48681; MUID: 94022386; PMID: 8415716
	A, Accession: A48681
	A; Molecule type: mRNA
•	A;Residues: 1-376 <cou></cou>
	A; Cross-references: GB: Z22658; NID: 9297411; PIDN: CAA80373.1; PID: 9297412
	A, Experimental source: placenta
	A, Note: authors translated the codon CAA for residue 198 as Gly
	R; Morgenstern, K.A.; Sprecher, C.; Holth, L.; Foster, D.; Grant, F.J.; Ching, A.; Kisie
	Biochemiatry 33, 3432-3441, 1994
	A)Title: Complementary DNA cloning and kinetic characterization of a novel intracellula:
	A; Merefence number: A54352; MUID: 94183847; PMID: 8136380
-	A Accession 1 A A 43.5.2
	Appropriate 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
_	A/Restaudes: 1-1/4/ E. 1.70-361/ 8/ 3663-376 < MONS > A/Restaudes: 1-1/4/ E. 1.70-361/ A. 1.70-3
	A.t.com:termines: ds:3092/2/ NID:3934008/; FIDN:4AB30320.1; FID:39340088
	A syperimental Bource: placenta
	A; Note: sequence extracted from NCBI backbone (NCBIN:145231, NCBIP:145232)
	R;Coughlin, P.B.; Tetaz, T.; Salem, H.H.
	J. Biol. Chem. 268, 9541-9547, 1993
	A, Title: Identification and purification of a novel serine proteinase inhibitor.
_	A; Reference number: A46672; MUID: 93252826; PMID: 8486644
	A;Accession: A46672
	A;Molecule type: protein
	A, Residues: 47-60;63-81;91-98 <co2></co2>
	A;Experimental source: placenta, leukemic cell line K562
	A, Note: sequence modified after extraction from NCBI backbone
	C; Genet 1CB:
	A;Gene: GDB:PI6
	A;Cross-reterences: GDB:252025; OMIM:173321
	A, Map position: 6p25-6p24.3
	C;Supertamily: antithrombin III
	C;Keywords: blocked amino end; cytosol; serine proceinase inhibitor
	r;341/11n1b1tory Bice: Arg (thrombin) #status predicted
	Query Match 35.3%; Score 404.5; DB 1; Length 376;
	best bocar simitarity   51.5%; Pred. No. 3.7e-30; Matches 85; Conservative 29; Mismatches 36; Indels 15; Gans 4;
	Qy 34 KARGKOLKOLIFF-PMSISSALAMVFMGAKGNIRAQMSQALCFSKIGGEDGDIHRGFGSL 92
	Db 1.7 KTT./ZPNS/KNV/PBCDM/KMC/21.3 M/V/W/C3/KGN/T3.5 OWN/CTT./CPNS/KNV/PBCDM/KMV/MC3/KGN/T3.5 OWN/CTT./CPNS/KNV/PBCDM/KNV/MC3/KGN/T3.5 OWN/KNV/KNV/KNV/KNV/KNV/KNV/KNV/KNV/KNV/KN

3,

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C;Accession: B59273
R;Sprecher, C.A.; Morgenstern, K.A.; Mathewes, S.; Dahlen, J.R.; Schrader, S.K.; Foster, D. Biol. Chem. 270, 29854-29861, 1995
A;Title: Molecular cloning, expression, and partial characterization of two novel member A;Reference number: A59273; MUID:96102039; PMID:8530382
A;Accession: B59273
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Residues: 1-376 <SPR>
A;Cross-references: GB:L40378; NID:g1160928; PIDN:AAC41940.1; PID:g1160929
A;Experimental source: tissue type placenta; note (vector lambda gt11); gene CAP2; tissu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Homo sapiens (man)
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 26-May-2000
C;Date: 23-Feb-1996 #sequence_revision 23-Feb-1996 #text_change 26-May-2000
C;Accession: 138202; S6675; S57522
R;Schneider, S.S.; Schick, C.; Fish, K.E.; Miller, E.; Pena, J.C.; Treter, S.D.; Hui, S Proc. Natl. Acad. Sci. U.S.A. 92, 3147-3151, 1995
A;Title: A serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication on A;Reference number: 138200; MUID: 95241462; PMID: 7724531
A;Accession: 138202
A;Status: nucleic acid sequence not shown
A;Molecule type: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leupin precursor - human
N/Alternate names: proteinase inhibitor 11 (PIII); squamous cell carcinoma antigen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 107 TANGLEGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKT--KAWKI 164
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            47 PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                                                                                                                                        79 GGE-DGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQ 137
                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    87
                                                 Gaps
                                                                                                                                         62
                                                                                              ----KQLKQLIFFPMSISSALAMVFMGAKGNTAAQMSOALCFSKI 78
                                                                                                                          C,Genetics:
A,Genetics:
A,Genetics:
C,Genetics:
A,Cross-references: GDB:599393; OMIM:601799
A,Map position: 6p25-6p25
C,Superfamily: antithrombin III
C,Superfamily: antithrombin Int
C,Keywords: proteinase inhibitor
F,340/Inhibitory site: Glu (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  . 9
                                                 19;
Length 378;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            proteinase inhibitor 9 - human
NyAlternate names: cytoplasmic antiproteinase 3 (CAP-3)
C;Species: Homo sapiens (man
C;bate: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 376;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                               Indels
                                                                                                                                                                                                                                                                                       138 LDFVNDTEKSTTRVNSWVADKTKAWKIIQTSLSHLEEPGIASS 180
                                                                                                                                                                                                                                                                                                                        43;
    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        11arity 46.3%; Score 320; DB 2;
Conservative 28; Mismatches 45.
  32.4%; Score 370.5; 2.47.2%; Pred. No. 5.7e-27
tive 24; Mismatches 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   : | :: | :: | 148 LPGSSIDAETRLVLVNAIYFKGKWNEP 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IQTSLSHLEEPGIASSSCYCKACLSQP 191
                                                      Conservative
                                                                                                      31 PFEKARG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Best Local Similarity
Matches 68; Conserv
                             Similarity
            Query ...
Best Local Simir
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       Query Match
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                                                                                                                                                                                                                                                                                                                                                     of the murine homologu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: GB:L40377; NID:g1160926; PIDN:AAC41939.1; PID:g1160927
A;Experimental source: tissue type placenta; note (vector lambda gt11); gene CAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           <u>ج</u>
                                                                                                                                                                                                                                                                                          Alternate names: cytoplasmic antiproteinase 2 (CAP-2)
Species: Homo sapiens (man)
Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Date: 08-Dec-1995 #sequence_revision 08-Dec-1995 #text_change 16-Jul-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVN 152
                                       76 LTEVNKTGTQYLLRVANRLFGEKSCDFLSSFRDSCQKFYQAEMEELDFISAVEKSRKHIN 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Residues: 1.378 <SUN>
A;Cross-references: GB:UZ5844; NID:g818902; PIDN:AAA79684.1; PID:g818903
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 13
C,Superfantly: antithrombin III
C,Keywords: serine proteinase inhibitor
F,343/Inhibitory site: Arg (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A,Map position: 18q21.3-18q21.3
C,Superfamily: antithrombin III
C,Keywords: proteinase inhibitor
F,339/Inhibitory site: Ang (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 374;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              tus: preliminary; not compared with conceptual translation
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                                                                                                                                      SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Accession: 857488

Sun, J.; Rose, J.B.; Bird, P.

1 Biol. Chem. 270, 16089-16096, 1995

Title: Gene structure, chromosomal localization, and exercise common structure, RMID: 95332310; PMID: 7608171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              34.3%; Score 392.5; DB 2; 52.9%; Pred. No. 4.9e-29; iive 23; Mismatches 34;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G-----KISEVLDAGTVDP-----LTKLVLVNAI 165
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   161 AWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GDB:599392; OMIM:601697
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      proteinase inhibitor Spi3 - mouse
C; Species: Mus musculus (house mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 34.3%
Best Local Similarity 52.9%
Matches 83; Conservative
                                                                                                                                                                                                                                                                           proteinase inhibitor 8 - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1-374 <SPR>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Status: preliminary A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Gene: GDB: PI8; CAP2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lecule type: mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Residues:
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                 93
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12;

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A;Residues: 1-350, 'G',352-356,'A',358-390 <5UM1>
A;Cross_references: GB:S66896; NID:g239551; PIDN:AAB20405.1; PID:g239552
A;Access_non: J10967
A;Access_non: J10967
A;Residues: 11-21;231-237;240-256;303-325 <5UM2>
C;Comment: This antigen probably acts as a proteinase inhibitor to modulate the host i. C;Genetics: GBs:SCCA1; SCC
A;Gene: GBB:SCCA1; SCC
A;Gene: GBB:SCCA1; SCC
A;Acnes: GBB:SCCA1; SCC
A;Acnes: GBS:SCA1; SCC
A;Acnes: S5/3; 74/3; 117/3; 157/1; 204/3; 256/3
C;Superfamily: antithrombin III
C;Keywords: Cysteine proteinase inhibitor; glycoprotein
C;Keywords: Cysteine proteinase inhibitor; glycoprotein
F;55,93,171,376/Binding site: Carbohydrate (Asn) (covalent) #status predicted
F;354/Inhibitory site: Ser (cathepsin b) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein
A; Residues: 1-41, E', 43-335, VD', 326-379 < DUB2>
R; Kordula; T.; Dubin, A.; Schooltink, H.; Koj, A.; Heinrich, P.C.; Rose-John, S.
Biochem. J. 293, 187-193, 1993
A; Title: Molecular cloning and expression of an intracellular serpin: an elastase inhib
A; Reference number: S34062; MUID:93319507; PMID:7687128
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         structure and identification as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            leckocyte elastase inhibitor - horse
Nilternate names: plasminogen activator inhibitor-2 homolog
(5.9pecies: Equus caballus (domestic horse)
(5.9pecies: Equus caballus (domestic horse)
(5.9pecies: 1993 #sequence revision 18-Nov-1994 #text_change 02-Jun-2000
(5.9pecies: A121; A37276; $\overline{5}$34062
(5.9pecies: A2421; A37276; $\overline{5}$34062
(7.9pubin, A.; Travis, J.; Finghild, J.J.; Potempa, J.
(7.9pubin, A27, 6576-6583, 1992
(A)Title: Equine leukocyte elastase inhibitor. Primary structure and identifiant feference number: A42421; MUID:92202200; PMID:1551869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              80 GEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76 DRSGNVHHQFQKLLTEFNKSTDAYELKIANKLFGEKTYLFLQEYLDAIKKFYQTSVESVD 135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Residues: 1-379 <KOR>
A;Cross-references: GB:M91161; NID:g164240; PIDN:AAA97513.1; PID:g164241 C;Superfamily: antithrombin III
C;Keywords: serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 FEKARGKOLKOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: protein
A; Residues: 1.379 < DUB1>
A; Residues: 1.379 < DUB1>
A; Cross-references: PIDN: AABZ1885.1; PID: g247842
A; Experimental source: leukocyte
A; Note: sequence extracted from NCBI backbone (NCBIP:89849)
K; Dubin, A.; Travis, J.; Enghild, J.J.; Potempa, J.
Submitted to the Protein Sequence Database, December 1991
A; Reference number: A37276
A; Accession: A37276
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23.2%; Score 266; DB 2; 37.9%; Pred. No. 3.8e-17; iive 28; Mismatches 47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              22.4%; Score 257; DB 2;
46.5%; Pred. No. 2.6e-16;
iive 19; Mismatches 38;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                140 FVNDTEKSTTRVNSWVADKT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A, Status: preliminary
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Best Local Simil
Matches 53; (
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Matches
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          A;Cross-references: EMBL:U19576, GB:U19569; NID:g852466
R;Barnes, R.C.; Worrall, D.M.
FEBS Lett. 373, 61-65, 1995
A;Title: Identification of a novel human serpin gene; cloning sequencing and expression A;Reference number: S66675; MUID:96013897; PMID:7589435
A;Accession: S66675
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*Scatus: preliminary; translated from GB/EMBL/DDBJ

*Molecule type: mRNA

**Residues: 1-350, 'G', 352-390 <SIL>

**Cross-references: EMBL:U19556; NID:g1276435; PID:g1052869

**Suminami, Y: Kishi, F:; Sekiguchi, K:; Kato, H.

**Suminami, Y: Kishi, F:; Sekiguchi, K:; Kato, H.

**Siochem. Biophys. Res. Commun. 181, 51-58, 1891

**Arfitle: Squamous cell carcinoma antigen is a new member of the serine protease inhibito
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                squamous cell carcinoma antigen 1 - human
C.Species: Homo sapiens (man)
C.Species: Homo sapiens (man)
C.Saces 23-Feb-1996 #sequence revision 23-Feb-1996 #text_change 26-May-2000
C.Saces 13201: 138201, G0631; JT0966; JT0967
R.Schneider, S.S.; Schick, C.; Fish, K.E.; Miller, E.; Pena, J.C.; Treter, S.D.; Hui, S.
Proc. Natl. Acad. Sci. U.S.A. 92, 3147-3151, 1995
Fles. A serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ï
                                                                                                                                                                                                    A; Molecule type: mRNA
A; Residues: 7-351, 'V', 353-384 <BAR>
A; Cross-references: EMBL: X89015; NID: 9887464; PIDN: CAA61420.1; PID: 9887465
C; Genetics: A; Genetics: BMBL: X89015; NID: 9887464; PIDN: CAA61420.1; PID: 9887465
C; Genetics: A; Genetics: BMBL: X89015; NID: 987464; PIDN: CAA61420.1; PID: 9887465
A; Genetics: A; Genetics: BMB: 36556; OMIM: 600518
A; Introns: 55/3; 74/3; 117/3; 157/1; 204/3; 256/3
A; Introns: 55/3; 74/3; 117/3; 157/1; 204/3; 256/3
C; Superfamily: antithrombin III
C; Superfamily: antithrombin III
C; Superfamily: affalue sequence #status predicted <NGP-
F; 1-22/Domain: Signal sequence #status predicted <NGP-
B) -384/Product: leupin #status predicted <NGP-
B) -376/Binding site: carbohydrate (Asn) (Covalent) #status predicted
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Molecule type: DNA
Residues: 1-117 <SCH2>
Cross-references: EMBL:U19562; NID:g897835; PIDN:AAA86316.1; PID:g897844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32 FEKARGKOLKQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG-----79
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Cross-references: EMBL:U19568; GB:U19558; NID:g1172085
Accession: 138200
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Submitted to the EMBL Data Library, January 1995
A/Reference number: G07968
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Best Local Similarity 38.64
Matches 54; Conservative
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Gaps

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plasminogen activator inhibitor 2 precursor - human NyAlternate names: urokinase inhibitor 2 precursor - human NyAlternate names: urokinase inhibitor C; Malternate names: urokinase inhibitor C; Malternate names: urokinase inhibitor 22-Nov-1989 #text_change 20-Oct-2000 C; Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 20-Oct-2000 C; Date: 22-Nov-1989 #sequence revision 22-Nov-1989 #text_change 20-Oct-2000 C; Date: 22-Nov-1989; M. J. Lebo, R. V.; Sadler, J.E. N. Ahern, S.M.; Le Beau, M.M.; Lebo, R. V.; Sadler, J.E. N. Ahern, S.M.; Le Beau, M.M.; Lebo, R. V.; Sadler, J.E. N. Ahern, S.M.; Le Beau, M.M.; Lebo, R. V.; Sadler, J.E. N. Aherne number: A32853; MUID:89174589; PMID:2494165 A; Recession: A32853 MUID:89174589; PMID:2494165 A; Recession: A32853 MUID:89174589; PMID:2494165 A; Recession: A1885 MID:89174589; PMID:2494165 A; Recession: A1886 MID:89174589; PMID:2494165 A; Recession: A1886 MID:90182678; PMID:2303256 A; Recession: 154218; MUID:90182678; PMID:2303256 A; Recession: 154218 A; Recession: 154218 A; Muid: GENEMBL/DDBJ A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; Recession: B42418 A; R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rispring, P.; Nakashima, T.; Frederick, M.; Henderson, Y.; Clayman, G. Biochem. Biochem. Biophys. Res. Commun. 264, 299-304, 1999
A; Title: Identification and cDNA cloning of headpin, a novel differentially expressed sheetence number. JC7118; MUID:99458661; PMID:10527881
A; Recession: JC7118
A; Racession: JC7118
A; Accession: JC7118
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A,Residues: 1-391 <SPR>
A,Cross-references: GB:AF169949; NID:g5911368; PIDN:AAD55765.1; PID:g5911369
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 26-May-2000
C;Accession: JC7118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         85 ----IHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
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                                                                                                                                                                                                          32 PFSISSAMAMVFLGTRGNTAAQLSKTFHFNIV----EEVHSRFQSLNADINKRGASYILK 87
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A,Map position: 18q21.3-18q22
C,Superfamily: antithrombin III
C,Keywords: serine proteinase inhibitor
F,355/Inhibitory site: Val (unidentified proteinase) #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24;
                                                                                                                                                                                                                                                                                                                                                                              107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK
Length 379;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19.6%; Score 224; DB 2; L 32.7%; Pred. No. 3.4e-13; Micmatches 54;
                                                                                    38;
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    Score 240; DB:
Pred. No. 1e-14;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             headpin serine proteinase inhibitor - human
                                                                                        23;
            21.0%;
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Best Local Similarity 32.7%
Matches 53; Conservative
                                                                                        Conservative
            Query Match
Best Local Similarity
Matches 49; Conserv
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A.Molecule type: mRNA
A.Molecule type: mRNA
A.Residues: 1-379 < REBA.
A.Fresidues: 1-379 < REBA.
B.Z.: Lee, S.S.: Remold-O'Donnell, E.; Komoriya, A.
B.Z.: Lee, S.S.: Remold-O'Donnell, E.; Komoriya, A.
A.Trile: A serpin from human tumor cells with direct lymphoid immunomodulatory activity:
A.Reference number: S65750; MUID:96049524; PMID:7578269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6 is inconsistent with that from Fig. 5 in having 256-Asq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Sep-1997
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 05-Sep-1997
C;Date: 13-Jan-1995 #sequence_revision 07.3 Alberts, M.
mold-O'Donnell, E.; Chin, J.; Alberts, M.
Mold-O'Donnell, E.; Chin, J.; Alberts, M.
A;Title: Sequence and molecular characterization of human monocyte/neutrophil elastase A;Reference number: S27383; MUID:92302296; PMID:1376927
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3;
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A;Atatus: preliminary
A;Atatus: preliminary
A;Molecule type: protein
A;Molecule type: protein
A;Residues: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;216-244;255-271,'X',273-274;291-301
C;Genetics: 57-69;97-110;111-129;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204-213;204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   serpin - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Species: Sus scrofa domestica (domestic pig)
C;Species: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 02-Jul-1998
C;Accession: S38962
R;Teschauer, W.F.; Mentele, R.; Sommerhoff, C.P.
R;Teschauer, W.F.; Mentele, R.; Sommerhoff, C.P.
A;Title: Primary structure of a porcine leukocyte serpin.
A;Reference number: S38962; MUID:94039085; PMID:7901009
A;Accession: S38962
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               107 TANGLEGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTKAWKIIQ 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  32 PFSISSALAMILLGTRGNTEAQMSKALHFDTV----KDIHSRFQSLNADINKCGASYLLK 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                       PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                     107 TANGLEGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 378;
                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 255.5; DB 2;
Pred. No. 3.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    27; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22.3%;
39.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 atus: preliminary
lecule type: protein
Ayeaidues: 1-778 <TES-
AyNote: the sequence from Fig. 6
C; Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        59; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     elastase inhibitor - human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
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F;23-415/Product: plasminogen activator inhibitor 2 #status predicted <MAT>
F;23/Modified site: acetylated amino end (Ser) (in mature form) #status predicted
F;5,115,1315/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;83,84,86/Cross-link: isopeptide (Gln) (interchain to Lys N6-amino of unidentified prot
F;380-381/Cleavage site: Arg-Thr (plasminogen activator) #status experimental
F;380/Inhibitory site: Arg (plasminogen activator) #status experimental
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A; Residues: 1-415 <BEL>
A; Cross-references: EMBL:X16490; NID:953589; PIDN:CAA34507.1; PID:953590
A; Cross-references: EMBL:X16490; NID:953589; PIDN:CAA34507.1; PID:953590
EMBO J. 8, 3287-3294, 1989
A; Title: Facultative polypeptide translocation allows a single mRNA to encode the A; Reference number: 809615; MUID:90059920; PMID:2583099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Species: Mus musculus (house mouse)
Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 16-Jul-1999
Accession: S20047; S09616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      bomapin - human
N;Alternate names: proteinase inhibitor 10 (PI10)
C;Species: Homo sapiens (man)
C;Date: 01.Mar-1996 #sequence_revision 01-Mar-1996 #text_change 16-Jul-1999
C;Accession: 139184
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    80 GFMQQIQKGSYPDAILQAQAADKIHSSFRSLSSAINASTGNYLLESVNKLFGEKSASFRE 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              74 ENFSGCDFAQQIQKENYPSAILQAQAGDKIHSAFSSLSSTINTPQGDYLLESANKLFGEK 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ---GEDGD-IHRGFQSLLVAINRTDTEYVLRTANGLFGEK 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             :| ||::| |::| ||::|| ||::|| ||::|| LKQIEKSNSTQ--NIFISPWSISSTLAIVLLGAGGNTEQQMAKVLQFNEIGSYGITTRNP 73
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 ------GEDGD------IHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20 AKASPTQNLFLSPWSISSTMAMVYMGSRGSTEDOMAKVLQFNEVGANAVTPMTPENFTSC
                                                                                                                                                                                                                                                                                                                               DB 2; Length 415;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 415;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SYDFLIGFIDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            / Match 19.3%; Score 221.5; DB 2; Local Similarity 32.1%; Pred. No. 6.2e-13; Ne 51; Conservative 27; Mismatches 48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    18.9%; Score 216.5; DB 2; ilarity 32.7%; Pred. No. 1.8e-12; Conservative 23; Mismatches 53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    submitted to the EMBL Data Library, September 1989 A;Reference number: $20047 A;Accession: $20047
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           122 GFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasminogen activator inhibitor 2 - mouse C;Species: Mus musculus (house mouse) (5,Date: 07-Apr-1994 #sequence_revision 07-C;Accesion: S20047; S09616 R;Belin, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Cross-references: EMBL:X16490
C; Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-27 <BEL2>
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Matches 54; Conserv
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A) Geule type: protein

A) Geule type: protein

A) Geule type: protein

A) Geule type: protein

A) Afisto. U. Kaudewitz, H.; Henschen, A.; Astedt, B.; Kruithof, E.K.O.; Bachmann, F. Fisto. U.; Kaudewitz, H.; Henschen, A.; Astedt, B.; Kruithof, E.K.O.; Bachmann, F. Fisto. U.; Kaudewitz, B.; 1988

A) Till: Determination of intermediates, products and cleavage site in the reaction betw A; Reference number: $02435; MUID:88167197; PMID:3280346

A) Accession: $02435; MUID:88167197; PMID:3280346

A) Accession: $02435; MUID:89167197; PMID:3280346

A) Residues: 15 Commun. 156, 383-388, 1988

A) Title: Plasminogen activator inhibitor 2. Isolation and characterization of the promot A; Reference number: 152229; MUID:89025873; PMID:2845977

A) Accession: 152229

A) Accession: Selection: Selection and Characterization of the promot A; Residues 1.55 RE2.

A) Accession: Selection: Selection: Selection and Characterization of the promot A; Residues: Selection and Selection: Selection and A; Residues Selection: Selection and A; Residues Selection: Selection and A; Residues Selection: Selection and Selection: Selection and A; Residues Selection: Selection and Selection and A; Residues Selection and Selection and A; Residues Selection and Selection and Selection and A; Introne: Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Selection and Select
                       A/Cross-references: GB:M31551; NID:g340152; PIDN:AAA36797.1; PID:g340154
FANtalia, T.M.; Clark, M.A.; Barnes, T.; Lehrbach, P.R.; Devine, P.L.; Schevzov, G.; GG
Proc. Natl. Acad. Sci. U.S.A. 885, 985-989, 1986
A;Title: Cloning and expression of a colna coding for a human monocyte-derived plasminoge
A;Reference number: A31366; MUD:88125032; PMID:3257578
A;Reselence number: A31366
A;Nolecule cype: mRNA
A;Residues: 1-415 <ANT-
A;Residues: 1-415 <ANT-
A;Residues: 1-415 <ANT-
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A;Residues: 1-435 <ANT-
A;Reference number: A46543; MUID:87252928; PMID:3496414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-119,'D', 121-403,'K',405-412,'C',414-415 <SCH>
A; Cross-references: GB: MB18082, 'N.D: 9189562; PIDN:AAA60006.1; PID: 9189563
A; Ye, R.D.; Wun, T.C.; Sadler, J.E.
J. Biol. Chem. 262, 3718-3725, 1987
A; Title: CDNA cloning and expression in Escherichia coli of a plasminogen activator inhi
A; Reference number: A26553; MUID: 87137674; PMID: 3029122
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Search completed: May 20, 2003, 10:26:44
Job time : 46 secs
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R,Riewald, M.; Schleef, R.R.
J. Biol. Chem. 270, 26754-26757, 1995
A,Title: Molecular cloning of bomapin (potease inhibitor 10), a novel human serpin that A,Reference number: I39184; MUID:96070759; PMID:7592909
A,Reference number: I39184
A,Status: preliminary
A,Molecule type: mRNA
A,Residuse: 1-397 < RES>
A,Cross references: EMBL:U35459; NID:gl065408; PIDN:AAC50282.1; PID:gl065409
C,Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 plasminogen activator inhibitor 2 type A - rat
C;Species: Rattus norvegicus (Norway rat)
C;Species: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 16-Jul-1999
C;Accession: S19896
R;Grundmann, U; Rein, T
B;Grundmann, U; Rein, T
A;Description: Complete cDNA sequence encoding plasminogen activator inhibitor 2 type
A;Reference number: S19896
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C;Species: Gallus gallus (chicken)
C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_change 18-Jun-1999
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A;Residues: 1-416 <GRU>
A;Cross-references: EMBL:X64563; NID:g56834; PIDN:CAA45864.1; PID:g56835
C;Superfamily: antithrombin III
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21 BSAQG---KNIFFSSWSISTSLTIVYLGAKGTTAAQMAQVLQFNRDQGVKCDFESEKKRR
                                                                                                                                                                                                                                                                                                                                                                                             21;
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                                                                                                                                                                                                                                                                                                                                                   Length 397;
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C;Date: 17-Dec-1982 #sequence_revision 17-Dec-1982 #text_.
C;Accession: A01244
R;Heilig, R.; Muraskowsky, R.; Kloepfer, C.; Mandel, J.L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18.6%; Score 213; DB 2; L. 31.9%; Pred. No. 3.9e-12; ive 22; Mismatches 55;
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18.6%; Score 213.5; DB 3
Best Local Similarity 32.2%; Pred. No. 3.3e-12.
Matches 47; Conservative 34; Mismatches 4
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138 PQPVNFVEASDQIRKDINSWVERQTE 163
                                                                                                                                                                                                                                                                      A,Map position: 14q32.1-14q32.1
C,Superfamily: antithrombin III
C,Keywords: serine proteinase inhibitor
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A;Cross-references: GDB:636283
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A,Molecule type: DNA
A,Residues. 1.388 <HEI>
A,Cross.references: GB:U00922; GB:V00439; NID:G212899; PIDN:AAA68882.1; PID:G212900
C,Genetics:
   Nucleic Acids Res. 10, 4363-4382, 1982
A,Title: The ovalbumin gene family: complete sequence and structure of the Y gene.
A,Reference number: A01244; MUID:83014329; PMID:7122240
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                                                                                                                                                                                                                                                                                         serine proteinase inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          11;
                                                                                                                                                                                                                             */Junicous: 56/3; 73/3; 116/3; 156/1; 203/3; 255/3
C;Superfamily: antithrombin III
C;Keywords: glycoprotein; phosphoprotein; serine proteinase inhibito
F;74-121/Disulfide bonds: #status predicted
F;293/Binding site: carbohydrate (Asn) (covalent) #status predicted
F;345/Binding site: phosphate (Ser) (covalent) #status predicted
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30.1%; Pred. No. 8.3e-11;
tive 32; Mismatches 57;
4363-4382, 1982
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nes 43; Conserv
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GenCore version 5.1.4 p5 4578 Copyright (c) 1993 - 2003 Compugen\_Ltd.

OM protein - protein search, using sw model

May 20, 2003, 10:19:11 ; Search time 13 Seconds (without alignments) 685.955 Million cell updates/sec Run on:

US-09-912-628-7 1145 1 HELRSWAAARRTGAHRHGCS.....SIPKCNSPVTPHGMWXPPSL 215 Title: Perfect score: Sequence:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

112892 seqs, 41476328 residues : peq:

I number of hits satisfying chosen parameters:,

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Датараве :

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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KAP MOUSE ALAF CAVPO ALAT BOVIN CBG RABIT CPIG RAT CPIG RAT ALAT SHEBP BEP45 XENIA ALAT SHEBP BEP45 XENIA ALAT SHEBP ALAT
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15.9 15.8 15.8 15.6 15.3 15.3 15.3
181.5 181 181 180 178.5 178.5 175. 175. 173.5 173.5

## ALIGNMENTS

RESULT 1

PTI6 ID	HUMAN PTI6_HUN
AC	P35237; Q96J44;
E I	01-FEB-1994 (Rel. 28,
בים	15-JUN-2002 (Rel. 41, Last sequence update)
DE	rombin
DE	inhibitor 6) (PI-6).
SS	SERPINBE OR PIE OR PII.
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2 5	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
36	Primates;
R.	
RP	SEQUENCE PROM N.A.
RC	TISSUE=Placenta;
<b>X</b>	MEDLINE=94022386; PubMed=8415716;
3 F	Salem H.H.,
R	crounts and molecular characterization of a human intracellular Berine profesionage south but or ".".
F.	Proc. Natl. Acad. Sci. U.S. A. 90.9417-9421 (1993)
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RP	SEQUENCE FROM N.A., AND SEQUENCE OF 67-73 AND 144-149.
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ž :	PubMed=8136380;
\$ £	Morgenstern K.A., Sprecher C.A., Holth L., Foster D., Grant F.J.,
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ä	Richamistry 22.2422.2441/10041
Z.	(3)
ЯP	SEQUENCE FROM N.A.
RC	TISSUE=Colon;
æ	Strausberg R.;
R.	Submitted (DEC-2000) to the EMBL/GenBank/DDBJ darahases
႘	-!- FUNCTION: Inhibits thrombin.
ខ	-1- SUBCELLULAR LOCATION: Cytoplasmic.
ខ	-!- TISSUE SPECIFICITY: HIGHEST LEVELS IN SKELETAL MUSCLE. ALSO FOUND
ဗ္ဗ ဗ္ဗ	IN PLACENTA, CARDIAC MUSCLE, LUNG, LIVER, KIDNEY AND PA
38	-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
3 6	1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
3 5	herwoon the control and the copyright. It is produced through a collaboration
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žä	EMBL) BUOUL394; AAH01394.1; DIP: S15750. S25750
, K	PIR; A48681; A48681.
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Gaps

17;

Indels

Length 374;

DB 1;

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41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
Serpin; Serine protease inhibitor.
ACT SITE 339 340 REACTIVE BOND (BY SIMILARITY).
SEQUENCE 374 AA; 42786 MW; E855A033519AC60E CRC64;
                                                Query Match

34.3%; Score 392.5; DB 1

Best Local Similarity 52.9%; Pred. No. 7.7e-30;

Matches 83; Conservative 23; Mismatches 34.
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                                                                                                                                                                                                                                                                                            34 KARGKOLKOLIFF-PMSISSALAMVFWGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSL 92
                                                                                                                                                                                                                                            17 KTLGKDNSKONVFFSPMSMSCALAMVYMGAKGNTAAQMAQILSFNKSGG-GGDIHQGFQSL 75
                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 270:29854-29861(1995).
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Šerpin B8).
SERPINB8 OR PI8.
Homo sapiens (Human).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytoplasmic antiproteinase 2 (CAP2) (CAP-2) (Protease inhibitor
                                                                                                                                                                                                   15;
                                                                                                                                                                            DB 1; Length 376;
                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                               153 SWVADKTKAWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                                                                                               341 342 REACTIVE BOND.
175 175 = -> G (IN REF. 1).
362 362 S -> R (IN REF. 1).
376 AA, 42590 MW, 2846A55F40C608C6 CRC64;
                                                                                                                                                                           35.3%; Score 404.5; DB 1;
51.5%; Pred. No. 5.6e-31;
tive 29; Mismatches 36;
                                                                                                                                                                                                                                                                                                                                                                                                                          374 AA.
                                                                                                              REACTIVE BOND.
                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE=Placenta;
MEDLINE=96102039; PubMed=8530382;
                                                                                                     Serpin; Serine protease inhibitor
                        MIM; 601697; -. InterPro; IPR000215; Serpin. Pfam; PF00079; Serpin; 1. SMART; SM00093; SERPIN; 1. PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; L40377; AAC41939.1; -. HSSP; P05120; 1BY7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:8952; SERPINB8
                                                                                                                 342
175
362
                                                                                                                                                                                                         85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                           STANDARD;
                                                                                                                                                                              Query Match
Best Local Similarity
Matches 85; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SECUENCE FROM N.A.
              HSSP; P05120; 1BY7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inhibitors.
                                                                                                                                                                                                                                                                                                                                                                                                                           SPB8_HUMAN
                                                                                                                                          CONFLICT
                                                                                       PROSITE;
                                                                                                                    SITE
                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                SPB8_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          proteinases.";
Brain Res. 42:293-300(1996).
Brain Res. Mol. Brain Res. 42:293-300 (1996).
PRESENT IN THE BRAIN OR EXTRAVASATED FROM THE BLOOD.
SUBCELLUAR LOCATION: Cytoplasmic (By similarity).
ITSUB SPECIFICITY: BRAIN.
ITSUB SPECIFICITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                     101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                              26 RNVPFSPMSISSALAMVFMGAKGSTAAQMSQALCLYK----DGDIHRGFQSLLSEVNRTG 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=97165893; PubMed=9013786; Nakaya N., Nishibori M., Kawabata M., Saeki K.; Nishibori M., Kawabata M., Saeki K.; Cloning of a serine proteinase inhibitor from bovine brain: expression in the brain and characterization of its target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            33.9%; Score 388; DB 1; Length 378; 60.8%; Pred. No. 2.1e-29; tive 21; Mismatches 26; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    378 AA; 42560 MW; 664F499CCFCE263A CRC64;
                                                                                                                                                                        161 AWKIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                            30-WAY-2000 (Rel. 39, Created)
30-WAY-2000 (Rel. 39, Last sequence update)
30-WAY-2000 (Rel. 39, Last annotation update)
Serine proteinase inhibitor B-43.
Bos taurus (Bovine)
                                                                                                                                                                                                                                                                                                                                                                            378 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HSSP; PO5120; 1BY7.
InterPro; IPR00215; Serpin.
Plam; PF00079; Serpin; 1.
SMART; SW0009; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; D55670; BAA19875.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity 60.8
                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=9913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TISSUE=Brain;
                                                                                                                                                                                                                                                                                                                                                                                  PTI6_BOVIN
002739;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ACT SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                               RESULT 3
PTI6_BOVIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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25 KNVFISPLSISSALAMVLLGAKGNTAAQMCQTLSLNKSSGGGEDVHQGFQNLLSEVNRRD 84

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47 PMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation use Day non-profit institutions as long as its content is. in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lab-sib.ch).
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79 GGE-DGDIHRGFOSLLVAINRIDTEYVLRTANGLFGEKSYDFLTGFTDSCCKFYQATIKQ 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mus musculus (Mouse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                       STRAIN=BALB/c;
MEDLINE=9533310; PubMed=7608171;
Sun J., Rose J.B., Bird P.,
Gene structure, chromosomal localization, and expression of the murine homologue of human proteinase inhibitor 6 (PI-6) suggests divergence of PI-6 from the ovalbumin serpins.";
J. Biol. Chem. 270:16089-16096(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 378;
                                                                                                                                                              15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Placental thrombin inhibitor (Protease inhibitor 6) (PI-6)
SERPINB6 OR SPI3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Serpin; Serine procease inhibitor.
ACT SITE 343 344 REACTIVE BOND (BY SIMILARITY).
SEQÜENCE 378 AA; 42599 MW; 4B0F5ElA030BBDF6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         43; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   138 LDFVNDTEKSTTRVNSWVADKTKAWKIIQTSLSHLEEPGIASS 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32.4%; Score 370.5; DB 1
47.2%; Pred. No. 9.6e-28;
tive 24; Mismatches 43
                                                                                                                                        378 AA.
                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MGD; MGI:103123; Serpinb6.
InterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EMBL; U25844; AAA79684.1; -. EMBL; BC006766; AAH06766.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ouery Match
Best Local Similarity 47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pfam, PF00079; serpin, 1.
SMART, SM00093; SERPIN, 1.
PROSITE, PS00284; SERPIN,
                                                                                                                                    STANDARD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
TISSUE=Breast tumor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PO5120; 1BY7.
                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                    CBI_TaxID=10090;
                                                                                                                                PTI6 MOUSE
Q60854;
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SEQUENCE
                                                                                                            PTI6_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 63
                                                                                                                              STEEPER SOOG STEEPER STEEPER STEEPER STEEPER SOOG STEEPER STEEPER SOOG STEEPER STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEEPER SOOG STEE
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7
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MEDLINE=97066975; PubMed=8910377;
MEDLINE=97066975; PubMed=8910377;
Sun J. Bird C.H., Sutton V., McDonald L., Coughlin P.B., Jong T.A.,
Trapani J.A., Bird P.I.;
"A cytosolic granzyme B inhibitor related to the viral apoptotic
regulator cytokine response modifier A is present in cytotoxic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T WO
                                                                             01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Cytoplasmic antiproteinase 3 (CAP3) (CAP-3) (Protease inhibitor 9)
                                                                                                                                                                                                                   Homo sapiens (Human).
Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (REB-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: GRANZYME B INHIBITOR.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of
                                                                                                                                                                                                                                                                                                                                                                                                                                                Sprecher C.A., Morganstern K.A., Mathewes S., Dahlen J.R., Schrader S.K. Foster D.C., Kisiel W.; Molecular cloning, expression, and partial characterization novel members of the ovalbumin family of serine proteinase inhibitors."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REACTIVE BOND (BY SIMILARITY)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 27.9%; Score 320; DB 1; Length 37; Best Local Similarity 46.3%; Pred. No. 6e-23; Matches 68; Conservative 28; Mismatches 45; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ECBA80869B939753 CRC64;
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     376
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Biol. Chem. 270:29854-29861(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lymphocytes.",
J. Biol. Chem. 271:27802-27809(1996),
                                                                                                                                                                                                                                                                                                                                                                                          TISSUE=Placenta;
MEDLINE=96102039; PubMed=8530382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Serpin, Serine protease inhibitor.
ACT SITE 340 341 REACT
                                                        Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; L40378; AAC41940.1; -. EMBL; U71364; AAC50793.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro; IPR000215; Serpin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BC002538; AAH02538.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Genew; HGNC:8955; SERPINB9.
STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pfam; PF00079; serpin; 1
SMART; SM00093; SERPIN;
                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
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                                                                                                                                                              (Serpin B9).
SERPINB9 OR P19.
                                                                                                                                                                                                                                                                                                          NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Strausberg R.;
                                                     01-OCT-1996
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SPB9 HUMAN
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X89015; CAA61420.1;
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SEQUENCE
                                                                                                PROSITE;
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 EMBL;
EMBL;
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                       EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE=21167379; PubMed=11267667; MEDLINE=21167379; Hamada K., Shinomiya H., Agano Y., Kihana T., Iwamoto M., Hirose S., Kyo S., Ito M.; Hashimoto K., Hirose S., Kyo S., Ito M.; Molecular cloning of human squamous cell carcinoma antigen 1 gene and
                         TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWYADKT--KAWKI 164
                                      Barnes R.C., Worrall D.M.; "Identification of a novel human serpin gene; cloning sequencing and
   32 PVSISSALAMVLLGAKGNTATQMAQALSLN----TEEDIHRAFQSLLTEVNKAGTQYLLR 87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=95241462; PubMed=7724531;
Schneider S.S., Schick C., Fish K.E., Miller E., Pena J.C.,
Treter S.D., Hui S.M., Silverman G.A.;
"A serine proteinase inhibitor locus at 18q21.3 contains a tandem
duplication of the human squamous cell carcinoma antigen gene.";
Proc. Natl. Acad. Sci. U.S.A. 92:3147-3151(1995).
                                                                                                                                                                                                                                  Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                           01-OCT-1996 (Rel. 34, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Squamous cell carcinoma antigen 2 (SCCA-2) (Leupin)
SERPINB4 OR SCCA2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 characterization of its promoter.";
Biochim. Biophys. Acta 1518:124-131(2001)
                                                                                    148 LPGSSIDAETRLVLVNAIYFKGKWNEP 174
                                                                      165 IQTSLSHLEEPGIASSSCYCKACLSQP 191
                                                                                                                                                   PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     U19571; AAA92602.1; JOINED.
U19572; AAA92602.1; JOINED.
U19574; AAA92602.1; JOINED.
U19575; AAA92602.1; JOINED.
U19575; AAA92602.1; JOINED.
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                                                                                                                                                                         01-FEB-1996 (Rel. 33, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U19576; AAA92602.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                expression of leupin."; FEBS Lett. 373:61-65(1995).
                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                             Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ISSUE=Bone marrow;
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SCC2_HUMAN
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: MAY ACT AS A PROTEASE INHIBITOR TO MODULATE THE HOST
-!- FUNCTION: TUNOR CELLS.
-!- SUBCELLULAR LOCATION: Cytoplasmic.
-!- TISSUB SPECIFICITY: SQUAMOUS CELLS.
-!- TISSUB SPECIFICITY: SQUAMOUS CELLS.
-!- DEVELOPMENTAL STAGE: ITS EXPRESSION IS CLOSELY RELATED TO CELLULAR
-!- DIFFERENTIATION IN BOTH NORMAL AND MALIGNANT SQUAMOUS CELLS.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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SEQUENCE FROM N.A.
MEDLINE=95241462; PubMed=7724531;
MEDLINE=95241462; PubMed=7724531;
Schneider S.S., Schick C., Fish K.E., Miller E., Pena J.C.,
Treter S.D., Hui S.M., Silverman G.A.;
Treter S.D., Hui S.M., Silverman G.A.;
A scrine proteinase inhibitor locus at 18q21.3 contains a tandem a serine proteinase inhibitor locus at 18q21.3 contains a tandem duplication of the human squamous cell carcinoma antigen gene.";
duplication of the human squamous cell carcinoma antigen gene.";
Proc. Natl. Acad. Sci. U.S.A. 92:3147-3151(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          80 GEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD
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Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
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                                                                                                                                                                                                                                                                                                                                                                                                                                             12;
                                                                                                                                                                                                                                                                                                                                                                             Length 390;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P29508 (096121)
01-ARR-1993 (Rel. 25, Created)
15-UNN-2002 (Rel. 41, Last sequence update)
15-UNN-2002 (Rel. 41, Last annotation update)
Squamous cell carcinoma antigen 1 (SCCA-1) (Protein T4-A)
SERPINB3 OR SCCA1 OR SCCA.
                                                                                                                                                                                                                                                                                                                                                                                                                                             47; Indels
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                                                                                                                                                                                                                                                                                                                   390 AA; 44854 MW; 04E213CD892587D5 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ochem. Biophys. Res. Commun. 181:51-58(1991)
                                                                                                                                                                                                                                                                                                                                                                                23.8%; Score 272; DB 1;
38.6%; Pred. No. 2.3e-18;
tive 27; Mismatches 47
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ACT_SITE 354 355 REACT
AB035089; BAB21525.1; -. BC017401; AAH17401.1; -.
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136 FANAPEESRKKINSWVESQT 155
                                                                                                                                   InterPro; IPR000215; Serpin.
                                                                                   Genew; HGNC:10570; SERPINB4
                                                                                                                                                                                                                                                                                                                                                                                                                                                54; Conservative
                                                                                                                                                                         Pfan, PF00079; serpin; 1. SMART; SM00093; SERPIN; 1. PROSITE; PS00284; SERPIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                      HSSP, PO1008; 1ATH
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                                                                                                                      MIM; 600518; -
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between the Swiss Institute of Bioinformatics and the EMBL outstation-
the Buropean Bioinformatics Institute. There are no restrictions on its
use by non-profit institutions as long as its content is in no way
modified and this statement is not removed. Usage by and for commercial
entities requires a license agreement (see http://www.isb-sib.ch/announce/
or send an email to license@lsb-sib.ch)
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01-NOV-1988 (Rel. 28, Last sequence update)
16-OCT--2001 (Rel. 40, Last annotation update)
Leukocyte elastase inhibitor (LEI).
SERPINBI OR ELANH2.
Equus caballus (Horse).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata; Euteleostomi, Mammalia; Eutheria; Perissodactyla; Equidae; Equus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23.2%; Score 266; DB 1; Length 390; and 37.9%; Pred. No. 8.46-18; Conservative 28; Mismatches 47; Indels
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MEDLINE=93119507; PubMed=7687128;
Kordula T., Dubin A., Schooltink H., Koj A., Heinrich P.C.,
Rose-John S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                              354 355 REACTIVE BOND.
357 357 T -> A (IN REF. 1).
390 AA; 44564 MW; ESF27F986C752CFA CRC64;
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AAA86317.1; JOINED.
AAA86317.1; JOINED.
AAA86317.1; JOINED.
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EMBL; U19556; AAA97552.1;
EMBL; U19559; AAA86317.1;
EMBL; U19559; AAA86317.1; JOINE
EMBL; U19560; AAA86317.1; JOINE
EMBL; U19565; AAA86317.1; JOINE
EMBL; U19565; AAA86317.1; JOINE
EMBL; U19567; AAA86317.1; JOINE
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136 FANAPEESRKKINSWVESQT 155
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TISSUE=Leukocyte;
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R. MEDLINE-SCOROLO; Pubble 13.; Proceeps J.; Public C. Prinary structure and public Scorolo; Pubble 13.; Pravis D.; Engelild J.; Proceeps J.; Public A.; Travis D.; Engelild J.; Proceps J.; Public A.; Pravis D.; Engelild J.; Public C.; Public A.; Parcolo L.; Public C.; Public A.; Maccock W.; Travis D.; Public C.; Public A.; Maccock W.; Travis D.; Public C.; Public A.; Maccock W.; Travis D.; Public C.; Public A.; Maccock W.; Travis D.; Public C.; Public C.; Maccock W.; Travis D.; Public C.; Public C.; Maccock W.; Pravis D.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.; Public C.;
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                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Treschauer W.F., Mentele R., Sommerhoff C.P.;

"Perchauer W.F., Mentele R., Sommerhoff C.P.;

"Primary structure of a porcine leukocyte serpin.";

Eur. J. Biochem. 217:519-526(1993).

"Ens. FUNCTION: REGULATES THE ACTIVITY OF THE NEUTROPHIL PROTEASE
ELSSTASE, CATHEREN G AND PROTEINASE-3 (By similarity).

"SUBUNIT: HOMODIMER; DISTULPIDE-LINKED.

"SUBUNIT: HOMODIMER; DISTURINE-LINKED.

"SUBULARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.

HSSP; P05619; IHLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-0cT-1993 (Rel. 27, Last sequence update)
16-0CT-2001 (Rel. 40, Last annotation update)
Leukocyte elastase inhibitor (LEI) (Leucocyte neutral proteinase
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                                                                                                                                                                                                                                                                                                                                        107 TANGLEGEKSYDFLIGETDSCGKEYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
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REACTIVE BOND (BY SIMILARITY).
3CA7C65F11E508CA CRC64;
                                                                                                                                                                                                                                      22.4%; Score 257; DB 1; Length 379; 46.5%; Pred. No. 5.8e-17; ive 19; Mismatches 38; Indels
                                                                                                                                                                                                                  72DED1999371427A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                  378 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Serpin; Serine protease inhibitor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Leukocyte;
MEDLINE=94039085; PubMed=7901009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  42512 MW;
                                                                                                                                                                                                                      43006 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN;
                                                                                                                                                                                                                                               cy Match
Local Similarity 46.5%
Thes 53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
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                                                                                                                                                                                                                       379 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9823;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sus scrofa (Pig)
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SEQUENCE
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Best Local
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ID TLEU PIG
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Gaps

Conservative

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=92302296; PubMed=1376927;
Remold-O'Donnell E., Chin J., Alberts M.;
"Sequence and molecular characterization of human monocyte/neutrophil
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. SEQUENCE FROM N.A. SEQUENCE FROM N.A. Remold-O'Donnell E.;
Zeng W., Silverman G.A., Remold-O'Donnell E.;
"Structure and sequence of human M/NEI (monocyte/neutrophil elastase inhibitor), an Ov-serpin family gene.";
Gene 213:179-187(1998).
                                                                                                                                                                           "Microsequences of 145 proteins recorded in the two-dimensional gel microsequences of normal human epidermal keratinocytes."; protein database of normal human epidermal keratinocytes."; protein database of normal human epidermal keratinocytes."; electrophoresis 13:960-969(1992).

Electrophoresis 13:960-969(1992).

Electrophoresis 13:960-969(1992).

ELASTARE, CATHERSIN G AND PROTEINASE-3.

ELASTARE, CATHERSIN G AND PROTEINASE-3.

ELASTARE, CATHERSIN G AND PROTEINASE-3.

SUBCELLULAR LOCATION: Cytoplasmic (By similarity).

SUBCELLULAR BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
PMSISSALAMVEMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                                                                                    107 TANGLEGEKSYDFLIGFIDSCGKFYQATIKQLDFVNDIEKSTIRVNSWVADKIKAWKIIQ 166
                                          32 PFSISSALAMILLGTRGNTEAQMSKALHFDTV----KDIHSRFGSLNADINKCGASYILK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Euteleostomi;
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01.APR-1993 (Rel. 25, Last sequence update)
15.Unv.2002 (Rel. 41, Last annotation update)
15.Unv.2002 (Rel. 41, Inst annotation update)
1eukocyte elastase inhibitor (LEI) (Monocyte/neutrophil elastase inhibitor) (M/NEI) (EI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutele
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Strausberg R., Submitted (MAY-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            elastase inhibitor.";
Proc. Natl. Acad. Sci. U.S.A. 89:5635-5639(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          379 AA
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                                                                                                                                                                                                                                                                                                                             143 -KIPELLASGVVDSA-----TKLVLVNAI 165
                                                                                                                                                                                                                                                                                  167 TSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
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EMBL; AP053630; AAC31394.1; -
EMBL; EC009015; AAH09015.1; -
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MEDLINE=93162043; PubMed=1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SERPINB1 OR ELANH2 OR PI2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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ILEU HUMAN
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                                                                                                                                                                                        47 PMSISSALAMVEMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTEYVLR 106
                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Genomic cloning, mapping, structure and promoter analysis of HEADPIN, a serpin which is down-regulated in head and neck cancer cells."; Blochim. Blophys. Acta 1492:441-446(2000).
                                                                                                                                                                                                      SEQUENCE FROM N.A. (ISOFORM 1).
MEDLINE-20461850; PubWed=11004515;
Nakashima T., Pak S.C., Silverman G.A., Spring P.M., Frederick M.J.,
Clayman G.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Spring P., Nakashima T., Frederick M., Henderson Y., Clayman G., "Identification and cDNA cloning of headpin, a novel differentially expressed serpin that maps to chromosome 18q.", Biochem. Blophys. Res. Commun. 264:299-304(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence, organization, chromosomal localization and alternative splicing of the human serine protease inhibitor gene hurpin (PII3), which is up-regulated in psoriasis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE-21213570; Pubmed-11313015;
Abts H.F., Welss T., Scheuring S., Scott F.L., Irving J.A., Michel
Bird P.I., Ruzicka T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Abtв Н.F., Welвв Т., Mirmohammadsadegh A., Koehrer K., Michel G.,
Ruzicka Т.;
                                                                                                                                                                         4,
                                                                                                                                                                                                                                      107 TANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                   SB13 HUMAN STANDARD; PRT; 391 AA.
GUIIVB; Q9UBM1; Q9UKGO; Q9HCX1;
16-OCT-2001 [Rel. 40, Created)
15-OCT-2001 [Rel. 40, Last sequence update)
15-JUN 2002 [Rel. 41, Last sequence update)
Hurpin (Hacdrin) (Serpin B13)
SERPINB13 OR P113.
Home septems (Human).
                                                                                                                                            21.0%; Score 240; DB 1; Length 379;
43.0%; Pred. No. 2.4e-15;
iive 23; Mismatches 38; Indels
                                                                                                         REACTIVE BOND (BY SIMILARITY)
                                                                                                        344 345 REACTIVE BOND (BY SIMILAR
379 AA, 42741 MW, BAAE08DFCBCDBCD3 CRC64;
                                           InterProj 1PR000215; Serpin.
Pfem; PF00079; serpin; 1.
SMART, SM00093; SERPIN; 1.
PROSITE; PS00204; SERPIN; 1.
Serpin; Serine procease inhibitor.
SEQUENCE 379 AA; 42741 WW; BAAEDI
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MEDLINE=99458661; Pubmed=10527881;
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           Aarhus/Ghent-2DPAGE; 4314; IEF.
Genew; HGNC:3311; SERPINB1.
MIM; 130135; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. (ISOFORM 1).
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                                                                                                                                                                   49; Conservative
 HSSP; PO5619; 1HLE
                                                                                                                                                      Local Similarity
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                                                                                                                                            Query Match
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Matches
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SB13_HUMAN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            4
Cell Biol. 20:123-131(2001). FUNCTION: May play a role in the proliferation or differentiation of keratinocytes.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          85 ----IHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gapa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ol Keralinocyces.
-!- SURGELLULAR LOCATION: Cytoplasmic.
-!- ALTERNATIVE PRODUCTS: 2 isoforms; 1 (shown here) and 2; are produced by alternative splicing.
-!- TISSUE SPECIFICITY: SKIN-SPECIFIC.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalja; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SMART; SM00093; SEKELN; ...
PROSITE; PS00284; SERFIN; ...
Serpin; Serine protease inhibitor; Alternative splicing.
ACT_SITE 356 357 REACTIVE BOND (BY SIMILARITY).
VARSPLIC 206 257 MISSING (IN ISOFORM 2).
CONFLICT 75 75 MISSING (IN REF. 4).
CONFLICT 75 75 MISSING (IN REF. 2).
CONFLICT 293 293 G -> S (IN REF. 2).
CONFLICT 297 297 G -> S (IN REF. 1; CAA04937).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19.6%; Score 224; DB 1; Length 391; 32.7%; Pred. No. 8.2e-14; tive 31; Mismatches 54; Indels ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 FVNDTEKSTTRVNSWVADKTKAWKIIQTSLSHLEEPGIASSS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL, AJ001696, CAA04935.2, EMBL, AJ001697, CAA04938.2, EMBL, AJ001698, CAA04937.1; EMBL, AF169949, AAD55765.1;
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InterPro; IPR000215; Serpin.
Pfan, PF00079; Serpin; 1.
PRINTS; PR00676; MASPIN.
SWART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; AF169949; AAD55765.1;
EMBL; AF216854; AAF72879.1;
EMBL; AJ278717; CAC03569.1;
HSSP; P05120; 1BY7.
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SERPINB2 OR PAI2 OR PLANH2.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MIM; 604445;
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Matches 53;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).

**MEDLINE=99148112; PubMed=10368272; Mardine D., Whittaker J.S., Harrop S.J., Jankova L., Coles M., Jardine D., Whittaker J.S., Gould A.R., Meister A., King G.C., Mabbutt B.C., Curmi P.M.G.; Gould A.R., Meister A., King G.C., Mabbutt B.C., Curmi P.M.G.; Freolution: implications for plasminogen activator inhibitor 2 at 2.0-A resolution: implications for serpin function."; Structure 7:43-54 (1999).

Structure 7:43-54 (1999).

THE MONOCYTE DERIVED PAI-2 IS DISTINCT FROM THE ENDOTHELIAL
                                                                                                                                       MEDLINE=88142852; PubMed=3325828; Schleuning W.-D., Medcalf R.L., Hession C., Rothenbuhler R., Shaw A., Kruithof B.K.O.; Medralf R.L., Hession C., Rothenbuhler R., Shaw A., Kruithof E.K.O.; Plasminogen activator inhibitor 2: regulation of gene transcription during phorbol ester-mediated differentiation of U-937 human histiocytic lymphoma cells.; Mol. Cell. Biol. 7:4564-4567(1987).
                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
MEDLINE=89174589; PubMed=2494165;
We R.D., Ahern S.M., le Beau M.M., Lebo R.V., Sadler J.E.;
Ye R.D., Ahern S.M., le fore for human plasminogen activator inhibitor-2.
| Structure of the gene for human plasminogen activator inhibitor-2.
The nearest mammalian homologue of chicken ovalbumin.";
J. Biol. Chem. 264:5495-5502(1989).
                                                                                                                                                                                                                                                                                                                                                                                                    Webb A.C., Collins K.L., Snyder S.F., Alexander S.J., Rosenwasser L.J., Eddy R.L., Shows T.B., Auron P.E.; "Human monocyte Arg-Serpin cDNA. Sequence, chromosomal assignment, and homology to plasminogen activator-inhibitor."; J. Exp. Med. 166:77-94(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=90152678; PubMed=2303256; Samia U.A., Alexander S.J., Horton K.W., Auron P.E., Byers M.G., Shows T.B. Jr., Webb A.C.; Chromosomal organization and localization of the human urokinase inhibitor gene: perfect structural conservation with ovalbumin."; pdenomics 6:159-167(1990).
                                     TISSUE-Placenta;
MEDIINE-87137674; PubMed=3029122;
Ye R. D., Wun T.-Z., Sadler J.E.;
"CDM, Cloning and expression in Escherichia coli of a plasminogen activator inhibitor from human placenta.";
J. Biol. Chem. 262:3718-3725(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 12-17; 103-108 AND 314-321.
MEDLINE=93162043; PubMed=1286667;
Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E.,
Vandekerckhove J.;
"Microsequences of 145 proteins recorded in the two-dimensional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Strausberg R.;
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Monocytes;
MEDLINE=88125032; PubMed=3257578;
                                                                                                                                                                                                                                                                                                                                                                                   TISSUE=Monocytes;
MEDLINE=87252928; Pubmed=3496414;
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                        FROM N.A.
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CELL-DERIVED PAI-1.
-!- SUBGELLULAR LOCATION: CYTOPLASMIC OR EXTRACELLULAR.
-!- PTM: THE SIGNAL SEQUENCE IS NOT CLEAVED.
-!- PTM: THE SIGNAL SEQUENCE TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /FTId=VAR 011744.
S -> C (IN DBSNP:6104).
/FTId=VAR 011745.
N -> Y (IN REF. 7).
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32.1%; Pred. No. 1.5e-13;
iive 27; Mismatches 46
                                                                                                                                                                                                                                                                                                     JOINED.
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AAA36797.1; -.
AAA36797.1; JOINED.
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AAA36797.1; JOINED.
AAA36797.1; JOINED.
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Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
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Genew; HGNC:8584; SERPINB2.
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AAA60348.1; J
AAA60348.1; J
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AAA60348.1;
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CAA68666.1
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A32853; A32853.
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M31550;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Facultative polypeptide translocation allows a single mRNA to encode the secreted and cytosolic forms of plasminogen activators inhibitor
                                                                                                                                                                                                                                                                                                                                       Bukaryota, Metazoa; Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
NCDI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-99110951; Pubmed-9892694;
Oudherty K.M., Pearson J.M., Yang A.Y., Westrick R.J., Baker M.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-34; 54-74; 89-115; 124-156; 163-237 AND 265-302 FROM
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-1- PTM: THE SIGNAL SEQUENCE IS NOT CLEAVED.
-1- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY
                                                                                                                                 PAI2 MOUSE STANDARD; PRT; 415 AA.
PI2388; O35687; Q9QWZ6; Q9QWQ0; Q9QWP9; Q9QWP8; Q9QWP7;
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                                                                                                                                                                                                                                                                                                                                                                                                                        EQUENCE OF 1-27 FROM N.A.
STRAIN=AKR; TISSUS=Myeloid;
MEDLINE=9005920; PubMed=2583099;
Bellin D., Wohlwend A., Schleuning W.-D., Kruithof E.K.O.,
Vassalli J.-D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (SEP-1989) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                               01-OCT-1989 (Rel. 12, Created)
01-OCT-1989 (Rel. 12, Last sequence update)
15-JUN-2012 (Rel. 41, Last annotation update)
Plasminogen activator inhibitor-2, macrophage (PAI-2).
Mus musculus (Mouse)
140 EYIRLCQKYYSSEPQAVDFLECAEEARKKINSWVKTQTK 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AJ000386; CAA04047.1; -INED.
AJ000384; CAA04047.1; JOINED.
AJ000385; CAA04047.1; JOINED.
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AF069685; AAD08916.1; -.
AF069684; AAD08916.1; JOINED.
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STRAIN=AKR; TISSUE=Myeloid;
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80 -------GEDGD-IHRGFQSLLVAINRTDTEYVLRTANGLFGEK 115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE-Bone marrow;
MEDLINE-96070759; PubMed=7592909;
Riewald M., Schleef R.R.;
"Molecular cloning of bomapin (protease inhibitor 10), a novel human serpin that is expressed specifically in the bone marrow.";
J. Biol. Chem. 270:26754-26757(1995).
-- FUNCTION: MAY PLAY A ROLE IN THE REGULATION OF PROTEASE ACTIVITIES DURING HEMATOPOIESIS.
-- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29 IKPFEKARGKQLKQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG-----
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Mammalia, Butheria, Primates, Catarrhini, Hominidae, Homo.
NCBI_TaxID=9606,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          18.9%; Score 216.5; DB 1; Length 415; 32.7%; Pred. No. 4.5e-13; ive 23; Mismatches 53; Indele 35;
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H -> Y.

H -> I.

S -> N.

A -> T (IN REF. 3 AND 4).

W, C4FC78C5C3CA7D8B CRC64;
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01-FEB-1996 (Rel. 33, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Bomapin (Protease inhibitor 10) (Serpin B10).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397 AA
AAD08917.1; -. AAD08917.1; JOINED.
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46291 MW,
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55
415 AA;
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les 54; Conserv
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2810 HUMAN

AC P48595;
DT 01-FEB-
DT 15-JUN.
DE SERPINE

CS HOMO 68

OC BURARIYO

OC MARMENI

OX NCBI T8

RP SEQUEN

RR HOLLINE

RA HEWALO

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This SMISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                             This SWISS-TROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   -----EDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQAT 134
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       78 MEPNLSNSEEIHSDFQTLISEILKPNDDYLLKTANALYGEKTYAFHNKYLEDMKTYFGAE 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi, Mammalia, Butheria, Rodentia, Sciurognathi, Muridae, Murinae, Rattus. NCBI TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21 BSAQG---KNIFFSSWSISTSLTIVYLGAKGTTAAQMAQVLQFNRDQGVKCDPESEKKRK 77
                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (BY SIMILARITY)

-- PTM: THE SIGNAL SEQUENCE IS NOT CLEAVED (BY SIMILARITY)

-- SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERRIN SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Grundmann U., Rein T.; the EMBL/GenBank/DDBJ databases.
Submitted (FEB-1992) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: PAI-2 INHIBITS UROKINASE-TYPE PLASMINOGEN ACTIVATOR.
-!- SUBCELLULAR LOCATION: CYTOPLASMIC OR EXTRACELLULAR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    33 EKARGKQLKQLIFFPWSISSALAMVFWGAKGNTAAQMSQALCFSKIGG------
     TISSUE SPECIFICITY: EXPRESSED SPECIFICALLY IN THE BONE MARROW SIMILARITY: BELONGS TO THE SERPIN FAMILY. OV-SERPIN SUBFAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                     21;
                                                                                                                                                                                                                                                                                                                                                                                                    DB 1; Length 397;
                                                                                                                                                                                                                        HISSP; PO5619; 1HLE.
Genew, HGKC18942; SERPINBIO.
MLM; 602058; -
InterPro; IPR000215; Serpin.
Pfam; PR00077; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
ACTORITE; PS00284; SERPIN; 1.
BEQÜENCE 397 AA; 45402 MW; BCE01246867154DF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01.APR-1993 (Rel. 25, Created)
01.APR-1993 (Rel. 25, Last sequence update)
16.OCT-2001 (Rel. 40, Last amotation update)
19. Instructor inhibitor-2, type A (PAI2A).
SERPINB2 OR PAI2 OR PLANH2.
                                                                                                                                                                                                                                                                                                                                                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                    18.6%; Score 213.5; DB 1
32.2%; Pred. No. 8.3e-13;
                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 32.2%; Pred. No. 8.3e-
tes 47; Conservative 34; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              135 IKOLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      : :: || ::: || :|: 138 PQPVNFVEASDQIRKDINSWVERQTE 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; X64563; CAA45864.1; -. PIR; S19896; S19896.
                                                                                                                                                                                                   EMBL; U35459; AAC50282.1; -.
HSSP; P05619; 1HLE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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------GDIHRGFOSLLVAINRTDT-EYVLRTANGLFGE 114
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                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                    29 IKPFEKARGKQLKOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGED----
                                        PROSITE, PS00284; SERPIN; 1.
Serpin; Serine protease inhibitor; Plasma; Plasminogen activation;
Glycoprotein; Signal.
                                                                                                        N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
N-LINKED (GLCNAC...) (POTENTIAL)
REACTIVE BOND (BY SIMILARITY).
2877EDFE6AF9BB1F CRC64;
                                                                                                                                                                                                                                      Length 416;
                                                                                                                                                                                                                                                                      55; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                            115 KSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (BY SIMILARITY)
                                                                                                                                                                                                                                    18.6%; Score 213; DB 1;
31.9%; Pred. No. 9.7e-13;
tive 22; Mismatches 55.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Search completed: May 20, 2003, 10:24:21
                                                                                                                                                                                                            47247 MW;
InterPro; IPR000215; Serpi.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                            Query Match
Best Local Similarity 31.99
Matches 53; Conservative
                                                                                                                                         228
262
402
402
381
381
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ACT SITE
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May 20, 2003, 10:19:47 ; Search time 94 Seconds (without alignments) 527.382 Million cell updates/sec
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1145
1 HELRSWAAARRTGAHRHGCS.....SIPKCNSPVTPHGMWXPPSL 215
GenCore version 5.1.4 p5 4578
Copyright (c) 1993 - 2003 Compugen_Ltd.
                                                                                                                                                                                                                                                                                                                                      Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                      671580 seqs, 206047115 residues
                                                                   - protein search, using sw model
                                                                                                                                                                                                                                                  BLOSUM62
Gapop 10.0 , Gapext 0.5
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Perfect score:
Sequence:
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries 9p\_human:\*
sp\_invertebrate:\*
sp\_mammal:\* 9p\_archea:\*
9p\_bacteria:\*
9p\_fung1:\* sp\_organelle:\* SPTREMBL\_21:\* sp\_mhc:\* Database :

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

sp\_phage: \*
sp\_plant: \*
sp\_rodent: \*
sp\_vants: \*
sp\_virus: \*
sp\_vertebrate: \*
sp\_vertebrate: \* sp\_rvirus:\*
sp\_bacteriap:\*
sp\_archeap:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

O08804 mus musculu O88400 mus musculu O98800 mus musculu O99byf7 homo sapien O89byf8 homo sapien O08797 mus musculu O88806 mus musculu O84041 mus musculu O94058 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94088 mus musculu O94388 mus musculu O94282 mus musculu Description SUMMARIES 008804 08VH00 008PF7 09BXF7 09BYF7 08VHP7 09DA27 09D105 09D105 09D105 09D105 09D105 09D105 09D105 09D105 09D105 09D105 09D105 \* Query Match Length DB Score 3.77.5 34.7.5 34.7.5 34.7.5 2. Result 

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210	204	196.5	194	191.5	190.5	190.5	190.5	188.5	187.5	187.5	187.5	187	186.5	186.5	186.5	186.5	186.5	185	1010	104	L 44. J	184	183.5	182.5	182.5	182	182	180.5	179
17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35	36	0 0	2	38	39	40	41	42	43	44	45

## ALIGNMENTS

SEQUENCE Query Match

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Matches

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Kaiserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M., McKaone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E., Ragoussis J., Bird P.I.;
Ragoussis J., Bird P.I.;
"Comparison of human chromosome 6p25 with murine chromosome 13 reveals a greatly expanded Ov-serpin gene repertoire in the mouse.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26 RNLFFCPMSVSSALAMVYLGAKGNTATQMSEVLGLS----GNGDVHQSFQTLLAEINKTD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
Suminami Y., Kishi F., Murakami A., Sakaguchi Y., Kato H.;
"Novel Forms of SCC Antigen Transcripts Produced by Alternative
                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUL-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                 Strausberg R.;
Submitted (MAR-2002) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protease; Serpin.
SEOUENCE 374 AA; 42150 MW; F8B2ABB47AA47378 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30.0%; Score 344; DB 11; 50.0%; Pred. No. 5.4e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            369 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               26; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Created)
                                                                                                                                                                                                                                                                                                                                           EMBL; U96703; AAB57815.2; -. BMBL; BC025121; AAH25121.1; -. MGD; MCI:894657; Spie. InterPro; IPR000215; Serpin. PRM, SM00093; Serpin; 1. SMART; SM00093; SERPIN; 1. PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AB046400; BAB40773.1; -.
HSSP; P01008; LATH
HSSP; P01008; LATH
Interpro; IPR00215; Serpin,
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-JUN-2001 (TYEMBLEEL 17, 01-JUN-2002 (TYEMBLEEL 17, SCCA2b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                161 AWKIIQTSLSHLEEPG 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     142 G-----KISEVLSPG 151
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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               Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                          SECUENCE FROM N.A.
                                                                 NCBI TaxID=10090;
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                                                                                                                             STRAIN=FVB/N;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
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Ragoussis J., Bird P.I.;
"Comparison of Human Chromosome 6p25 with Murine Chromosome 13 Reveals and Greatly Expanded Ov-Serpin Gene Repertoire in the Mouse.";
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL; AF425084; AAL65910.1;
Interpro; IPR00015; Serpin.
Fram; PR00079; Serpin.
Fram; PR00079; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100 DTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25 KWVFLSPISISSALVMVLLGAKGTTAIQITQALSLGKCSSSEDGDVHQGFQLLLSEVNKT 84
                                                                                                                                                                                     100 DTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKT 159
                                                                                                                                                                                                            3; Gaps
                                                                             Gaps
                                                                                                             99
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKI-GGEDGDIHRGFQSLLVAINRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                           41 KQLIFFPMSISSALAMVFWGAKGNTAAQMSQALCFSKIGGEDG-DIHRGFQSLLVAINRT
                                                                                                                                     25 RNVLFSPISVSSALAMVFMGAKĞTTASQMAQALSLDKCSGKGGRDVHQGFQSLLTETNKT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           008800 PRELIMINARY; PRT; 374 AA.
008800;
01-JUL-1997 (TrEMBLrel. 04, Created)
01-DC-2001 (TrEMBLrel. 19, Last sequence update)
01-DGC-2001 (TrEMBLrel. 21, Last annotation update)
serine proteinase inhibitor NK10 (Serine protease inhibitor 8).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   30.3%; Score 347.5; DB 11; Length 385; 48.0%; Pred. No. 2.5e-26; ive 25; Mismatches 49; Indels 3;
                                                                             3;
                                        Length 377;
                                                                             41; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00284; SERPIN; UNKNOWN 1.
SEQUENCE 385 AA; 43786 MW; 0820A8A26AEBB485 CRC64;
     9660E8F3A41EE47A CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                          33.0%; Score 377.5; DB 1.
50.7%; Pred. No. 2.5e-29;
ive 29; Mismatches 41
                                                                                                                                                                                                                                                                                                                                                                                               385 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           160 -- KAWKIIQTSLSHLEEPGIASSSCYCK 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              EDKIKELLSPGTIHSNTPLILVNAVYFK 172
                                                                                                                                                                                                                                                                  160 --KAWKIIQTSLSHLEEPGIASSSCYCK 185
                                                                                                                                                                                                                                                                                       145 EDKITELLSSGSVNSNTPLVLVNAIYFK 172
                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
           42535 MW;
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                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                 PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mus musculus (Mouse)
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           377 AA;
                                                             Local Similarity
tes 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=10090;
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Local Sim
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[1] SEQUENCE FROM N.A.
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                                                                                                                                                                              GEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
                                                                                                                                                                                                       32 FEKARGKQLKQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG------ 79
                                                                                                                                80 GEDGDIHRGFOSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLD 139
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Primates, Catarrhini, Hominidae, Homo.
                                                                              12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ch 23.8%; Score 272; DB 4; Length 369; slailarity 38.6%; Pred. No. 8.4e-19; 54; Conservative 27; Mismatches 47; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 338;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Match 23.2%; Score 266; DB 4; Length 33 Best Local Similarity 37.9%; Pred. No. 3e-18; Matches 53; Conservative 28; Mismatches 47; Indele
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     32 FEKARGKOLKOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIG----
   42287 MW; CED7A2426378DE3E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            338 AA; 38519 MW; SAB9CEF480ClABDF CRC64;
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Last annotation update)
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                                                                                                                                                                                                                                                       FUNDTEKSTTRVNSWVADKT 159
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136 FANAPEESRKKINSWVESQT 155
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SMART; SM00093; SERPIN; 1.
PROSITE; PS00284; SERPIN; 1.
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01-JUL-1997 (TrEMBLrel: 04,
01-JUL-1997 (TrEMBLrel: 04,
01-DEC-2001 (TrEMBLrel: 19,
Serine proteinase inhibitor
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   369 AA;
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SEQUENCE
 SEQUENCE
                                    Query Match
                                                       Local
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Q9BYF8;
                                                                        Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFGSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.; "A new family of ten murine ovalbumin serpins includes two homologs proteinase inhibitor 8 and two homologs of the granzyme B inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         4; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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: | | ||||:||||:||||:||||:|| | : :
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22.6%; Score 259; DB 11; Length 374; 46.7%; Pred. No. 1.7e-17; ive 23; Mismatches 37; Indels 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Serpin.
SEQUENCE 374 AA; 42259 MW; 76D9ED10D7875281 CRC64;
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EMBL: AF426025; AAL57487.1; -.
InterPro; IPR002016; Peroxidase.
InterPro; IPR002015; Serpin.
Fam; PF00079; Serpin; 1.
SMART; SM00093; SERPIN; 1.
PROSITE; PS00435; PERDYIN; 1.
PROSITE; PS00284; SERPIN; UNRXOWN 1.
SRQUENCE 382 AA; 42887 MW; 35GBBGADF677CBDB CRC64;
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Last annotation update)
                                                                                                                                                                                                                 382 AA.
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01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
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A Kawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A kawa J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A hakawa T., Hara A., Pukunishi Y., Konno H., Adachi J., Fukuda S.,
A hizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A shito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A sadto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
A radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A schriml L. Lewis S., Marsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Uyons P., Marchionni L., Mashima J., Mazarelli J., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Winnawa-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Warshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              82 NQKYCLIMANRLFVENTCELLPTFKESCLKFYHSEMEQLSFAEAAEBSRQHINMWVSKQT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    26 KNVCYSPMSISSALAMVLLGAKGDTAVQICQALHLN----PDEDVHQGFQLLLHNLNKQN 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
InxID=10090;
                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.7%; Score 248.5; DB 11; Length 377; 45.0%; Pred. No. 1.9e-16; ive 22; Mismatches 39; Indels 5;
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Last annotation update)
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Last annotation update)
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EMBL, AKO05394; BAB23998.1; -
HSSP, P05120; 1BY7.
MGD; MGI:1919260; 1600002F03Rik.
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Created)
                                                                                                                                                                                                                          STRAIN=C57BL/6J; TISSUE=PLACENTA;
MEDLINE=21085660; PubMed=11217851;
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InterPro; IPR000215; Serpin.
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                     (TrEMBLrel. (TrEMBLrel.
  (TrEMBLrel.
                       01-JUN-2001 (TrEMBLrel
01-JUN-2002 (TrEMBLrel
1600002F03Rik protein.
                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                  L600002F03RIK.
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01-MAR-2002 (
01-MAR-2002 (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NK21L1
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN=CS-TML/6J; TISSUE=ECTOPLACENTAL CONE; STRAIN=CS-TML/6J; Cadman M., Kaiserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman M., McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E., Ragoussis J., Bird P.I.; Comparison of human chromosome 6p25 with murine chromosome 13 reveals
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 101 TE-YVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
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STRAIN=C57BL/6J; TISSUB=ECTOPLACENTAL CONE;
MEDLINE=97326124; PubMed=9182575;
Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.;
sun J., new family of 10 murine ovalbumin serpins includes two homologs of proteinase inhibitor 8 and two homologs of the granzyme B inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                        Lukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
                                               103 YVLRTANGLEGEKSYDFLTGFTDSCGKFYQATIKOLDFVNDTEKSTTRVNSWVADKTKAW
      28 IFFSPFSISSSLAMVFLGAKGSTAAQLSKTLHFDSV----EDIHSCFQSLTAEVSKLGAS
                                                                         5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a greatly expanded Ov-serpin gene repertoire in the mouse."; Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.-:- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21.8%; Score 249.5; DB 11; Length 45.5%; Pred. No. 1.5e-16; ive 21; Mismatches 40; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         377 AA; 42783 MW; EC8C2D79916B2E4F CRC64;
                                                                                                                                                                                                                                                                                                                                         Last sequence update)
Last annotation update)
                                                                                                                                                              143 -----KIPELLAKGVVDS------MTKLVLVNAI 165
                                                                                                                                  163 KIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSI 197
                                                                                                                                                                                                                                                                               377 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [proteinase inhibitor 9).";
J. Biol. Chem. 272:15434-15441(1997).
                                                                                                                                                                                                                                                                                                                          Created)
                                                                                                                                                                                                                                                                                 PRT;
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Serine proteinase inhibitor NK26.
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InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
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                                                                                                                                                                                                                                                                                                                        (TrEMBLrel. 04, (TrEMBLrel. 19, (TrEMBLrel. 21,
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                                                                                                                                                                                                                                                                                   PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                              us musculus (Mouse)
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01-DEC-2001
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5

377 AA

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RESULT 9 Q9DAZ7

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PROSITE; PS00284; SERPIN; 1.
                                             Serpin.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              101 TB-YVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWYADKT 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            82 NOKYCLTMANRLEVENTCELLETFKESCLKFYHSEMEQLSFAEAAEESRQHINMWVSKQT 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN-C57BL/63; TISSUE-ECTOPLACENTAL CONE;
Kalserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E., Ragousaís J., Bird P.I.;
Comparison of Human Chromosome 6p25 with Murine Chromosome 13 Reve Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, AR455083, AAL55909 1;
Pfam; PF00079; serpin.
Pfam; PF00079; serpin.
PMRT; SMRQ15; SERPIN; I.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Lest sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
18 days embryo cDNA, RIKEN full-length enriched library,
                                                                                                                                                                                                                                                                                 PROSITE, PS00264; SERPIN; UNKNOWN 1.
SEQUENCE 377 AA; 42994 MW; CCA62840210BE40D CRC64;
                                                                                                                                                                                                                                                                                                                                     21.7%; Score 248.5; DB 11;
45.0%; Pred. No. 1.9e-16;
Mismatches 39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           387 AA.
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STRAIN-C57BL/6J; TISSUE=EMBRYO;
MEDLINE=21085660; Pubmed=11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MGD; MGI:1277952; Scca2.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM00093; SERPIN; 1.
                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity 45.08
Matches 54; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
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REARAWA T., Hara A., Flutunishi Y., Yoshino M., Itoh M., Ishii Y., Arakawa T., Hara A., Flutunishi Y., Konno H., Adachi J., Flutuda S., Arakawa T., Chazaki Y., Golobori T., Bono H., Kasukwa T., Saito R., Adacha K., Matsuda H.A., Ashburner M., Batalov S., Yamanaka I., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., Radota K., Matsuda H.A., Ashburner M., Batalov S., Gasvant T., Rohil P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J., Rohil P., Lewis S., Mateuo Y., Nikaido I., Pesole G., Quackenbush J., Sakai K., Okido T., Furuno M., Carninci M., Bansho T., Rabak J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Barak J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F., Rusha D., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H., Lyono P., Marchionni L., Mashima J., Mazzarelli J., Mombaerte P., Nordone P., Ring B., Ringwald M., Rodriguez I., Sakameto N., Sasaki H., Sato K., Schoenbach C., Seya T., Shipata Y., Storch K.-F., Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L., Manshiaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                               63 KKTTEKSEHCDDEENVHEQFQKLITQLNKSNDDYDLKAANSIYGAKGFPFLQTFLEDIKE 122
                                                                                                                                                                                                                                                                                                                                76 ----SKIGGEDGDIHRGFQSLLVAINRTDTEYVLRTANGLFGEKSYDFLTGFTDSCGK 129
                                                                                                                                                                                              24 KWHICIKPFEKARGKQL----KQLIFFPMSISSALAMVFMGAKGNTAAQMSQALCF--- 75
                                                                                                                                                                                                                                         3 RFHAADVKPAVEMYRQLRESDKNIFYSPISMMTALAMLQLGAKGUTEIQIEKVLQFIETT 62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                21.4%; Score 245; DB 11; Length 387; 32.0%; Pred. No. 4.5e-16; iive 37; Mismatches 60; Indels 20;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hayashizaki Y., "Functional annotation of a full-length mouse cDNA collection.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     130 FYQATIKQLDFVNDTEKSTTRVNSWVADKTKAWKIIQTSLSHLEEPGIASSS 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 21.2%; Score 243; DB 11; Length 379;
Best Local Similarity 34.5%; Pred. No. 6.9e-16;
Matches 58; Conservative 33; Mismatches 53; Indels 2:
387 AA; 44558 MW; AE25C02520F3B194 CRC64;
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Pfam; PF00079; serpin; 1.
PROSTIE; S800284; SERPIN; 1.
PROSTIE; P$00284; SERPIN; UNKNOWN 1.
SEQUENCE 379 AA; 42600 MW; 45B7BC6CE0816FD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
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SERPINBIA OR 1190005M04RIK.
Mus musculus (Mouse).
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                                                                                                    Local Similarity
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                                                             Query Match
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Matches
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09D154;

RESULT 13 Q9D154 ID Q9D15

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42575 MW; F492F1EEB88E80B1 CRC64;
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                                                                                                                       58; Conservative
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            379 AA;
                                                                      Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        008802
            SEQUENCE
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                                                                                                                                Matches
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CHAIN-CSTBL/6J; TISSUE=EMBRYO;

Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M.; Ishii Y.,

Kawai J., Shinagawa A., Falbata K., Yoshino M., Itoh M.; Ishii Y.,

Kawai J., Shinagawa A., Falbata K., Yoshino H., Adachi J., Fukuda S.,

Arakawa T., Hara A., Fukunishi Y., Konno H., Rondo S., Yamanaka I.,

A jizawa K., Izawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

A jizawa K., Isawa M., Nishi K., Kiyosawa H., Kando S., Yamanaka I.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaldo I., Pesole G., Quackenbush J.,

Ruehl P., Lewis S., Matsuo M., Ano H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Ano H., Baldarelli R., Barsh G.,

Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.,

Blake J., Boffelli D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazararelli J., Mombarts P.,

A sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

M. Wynshaw Boris B., Kinga K., Hasegawa Y., Kawaji H., Kohtsuki S.,

W. Warshavishi A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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                                                                            103 YVLRTANGLEGEKSYDFLIGFIDSCGKFYQATIKQLDFVNDTEKSTIRVNSWVADKIKAM 162
                                                                                                              STRAIN=CS-7BL/6J; TISSUE=SPLEEN; K.L., Gillard A., Mirza G., Cadman Kaiserman D., Knaggs S., Scarff K.L., Gillard A., Mirza G., Cadman McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E., Ragoussis J., Bird P.I.;
                  28 IPFSPFSISSALAMVILGAKGSTAAQLSKTFHFDSV----EDIHSRFQSLNAEVSKRGAS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
ammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                 163 KIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 210
                                                                                                                                                                                                                                      01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1190005M04Rik protein (RIKEN CDNA 1190005M04 gene) (EIA)
SERPINBIA OR 1190005M04RIK OR SERPINBI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strausberg R.;
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases
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EMBL; AK003930; BAB23079.1; -.
EMBL; BC011140; AAH11140.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                            379 AA
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InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (Mouse)
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PS00284; SERPIN;

SMART; SM00093; PROSITE; PS00284

EMBL

Serpin.

RA KAWAI J., Shingada K., Yoshino M., Itoh M., Ishii Y., RA KAWAI J., Shingada R., Shibata K., Yoshino M., Itoh M., Ishii Y., RA Arakawa T., Hara A., Shibata K., Komo H., Adachi J., Fukuda S., Ramanaka I., Razawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I., Ra Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Rastico T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R., Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T., RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T., RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G., RA Blake J., Bolfelli D., Boljunga N., Carninno P., de Bonaldo M.F., Ra Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M., RA Gustincich S., Hill D., Hofman M., Hume D.A., Kamiya M., Lee N.H., RA Lyons P., Marchionni L., Mashima J., Mazarelli J., Sakamoto N., RA Saski H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F., RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S., Havashizaki Y. STRAIN=CS7BL/G. Cadman M., STRAIN=CS7BL/G. Kaiserman D., Kanagas S., Scarff K.L., Gillard A., Mirza G., Cadman M., McKeone R., Denny P., Cooley J., Benarafa C., Remold-O'Donnell E., Ragoussis J., Bird P.I.;
"Comparison of human chromosome 6p25 with murine chromosome 13 reveals a greatly expanded Ov-serpin gene repertoire in the mouse."; STRAIN=CSTBL/6J; TISSUE=WHOLE EMBRYO;
STRAIN=57326124; PubMed=9182575;
MEDLINE=97326124; PubMed=9182575;
Sun J., Ooms L., Bird C.H., Sutton V.R., Trapani J.A., Bird P.I.;
"A new family of 10 murine ovalbumin serpins includes two homologs of proteinase inhibitor 8 and two homologs of the granzyme B inhibitor 103 YVLRTANGLEGEKSYDFLIGETDSCGKFYQATIKQLDFVNDTEKSTIRVNSWVADKTKAW 162 43 LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTE 102 Gaps 83 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus 28 IPFSPFSISSALAMVILGARGSTAAQLSKTFHFDSV----EDIHSRFQSLNAEVSKRGAS Functional annotation of a full-length mouse cDNA collection."; 24; , DB 11; Length 379; 6.9e-16; 163 KIIQTSLSHLEEPGIASSSCYCKACLSQPLLVHSIPKCNSPVTPHGMW 210 143 -----YEKGWUDS------YEKLVLVNAI------YEKGMW 171 Indels ol.-UUN-2002 (TrEMBLrel. 17, Last sequence update) 01.-UUN-2002 (TrEMBLrel. 21, Last annotation update) 1600019A21Rik protein (Serine proteinase inhibitor R86) 1600019A2IRIK. 377 AA 21.2%; Score 243; DB 34.5%; Pred. No. 6.9e ive 32; Mismatches Biol. Chem. 272:15434-15441(1997). 01-UUN-2001 (TrEMBLrel. 17, Created) 01-UUN-2001 (TrEMBLrel. 17, Last seq 01-UUN-2002 (TrEMBLrel. 21, Last ann PRT; SEQUENCE FROM N.A. STRAIN=C57BL/6J; TISSUE=PLACENTA; MEDLINE=21085660; PubMed=11217851; 

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Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,

Lawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Alto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Radota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,

Ruehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Rakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Bakai K., Okido T., Furuno M., Aono H., Mandarelli R., Manda C.,

Brownstein M.J., Bult C., Fletcher C., Fulita M., Gariboldi M.,

Lopos P., Marchioni L., Mashima J., Mazzarelli J., Mombaerts P.,

Nordone P., Ring B., Ringwald M., Rodríguez I., Sakamoto N.,

Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,

Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,

Hynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          41 KOLIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTD 100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             101 TEYVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKQLDFVNDTEKSTTRVNSWVADKTK 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   82 RKYSLIVANRLFADKTCEVLQTFKESCFRFYDSEMEGVNFFKAAVESRQCINTWVSKQTE 141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26 KNVCFSPVSISSALAMVLLGAKEQTAVQISQALGLKKEKG----IHQGFLKLLRKLNKPD 81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse).
Eukaryota, Metazoa, Chordata, Craniata, Vertebráta, Euteleostomi;
Mammalia, Eutheria, Rodentia, Sciurognathi, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              21.0%; Score 240; DB 11; Length 377; 43.3%; Pred. No. 1.4e-15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indela
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
-- SIMILARITY: BELONGS TO THE SERPIN FAMILY.
EMBL, AK005491; BAB24076.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                377 AA; 42733 MW; B6DCCAE1ADE932F4 CRC64;
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Last sequence update)
Last annotation update)
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EMBL; AKO08914; BAB25964.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    379 AA
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MEDLINE=21085660; PubMed=11217851;
                                                                                                                                                                 MGD, MGI:1919261; 1600019A21Rik.
InterPro; IPR000240; Magpin.
InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
                                                                                                   EMBL; U96705; AAB57817.2; -. HSSP; P05619; 1HLE.
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InterPro; IPR000215; Serpin.
Pfam; PF00079; serpin; 1.
SMART; SM0093; SERPIN; 1.
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SERPINBIA OR 1190005M04RIK.
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PROSITE; PS00284; SERPIN; 1
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Best Local Similarity 43.34
Matches 52, Conservative
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SMART; SM00093; SERPIN;
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                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE
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43 LIFFPMSISSALAMVFMGAKGNTAAQMSQALCFSKIGGEDGDIHRGFQSLLVAINRTDTE 102
                                                                                                                                                                            103 YVLRTANGLFGEKSYDFLTGFTDSCGKFYQATIKOLDFVNDTEKSTTRVNSWVADKTKAW 162
                                                                                                                                                                                                        84 HTLKLANRLYGEKTYNFLPEYLASTQKMYGADLAPVDFLHASEDARKEINQWVKGQTEG- 142
                                                                                                                                  24;
                                                  Length 379;
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                                                                                                                                                                                                                                                                     143 -----YPKGWDS------WTKLVLVNAI-----YPKGMW 171
                                                                                   Indels
               42580 MW; 193728585077AB4B CRC64;
                                                                                   55,
                                             20.7%; Score 237; DB 11;
33.9%; Pred. No. 2.7e-15;
iive 32; Mismatches 55;
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               379 AA;
                                                              Local Similarity
Serpin.
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Matches
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